GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 17:32:40 ; Search time 183.78 Seconds
(without alignments)
134.791 Million cell updates/sec

Title: US-09-540-843-5
Perfect score: 11
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	11	100.0	11	18	AAV07769	N3 to P5 oligonucl
c	2	11	100.0	11	18	AAT89250	DNA oligonucleotid
	3	11	100.0	11	18	AAT89237	Peptide nucleic ac
	4	11	100.0	11	18	AAT90060	Telomerase primer.
	5	11	100.0	11	21	AAA37556	PNA sequence #13 u
	6	11	100.0	11	21	AAA37561	PNA sequence #18 u
	7	11	100.0	11	21	AAA37562	PNA sequence #19 u
c	8	11	100.0	11	21	AAA37573	PNA sequence #31 u
	9	11	100.0	11	21	AAA37586	Antisense sequence
	10	11	100.0	11	22	AAF81185	Oligonucleotide th
	11	11	100.0	11	22	AAH26728	Phosphoramidate-li
	12	11	100.0	11	22	AAH26732	Phosphoramidate-li
	13	11	100.0	11	23	AAS14909	Melanogenesis asso
c	14	11	100.0	11	23	AAS14913	Melanogenesis asso
	15	11	100.0	11	23	AAS15434	PNA 7/IV inhibitin
c	16	11	100.0	11	23	AAS15450	Oligonucleotide #6
	17	11	100.0	11	23	AAS15457	Phosphorothioate (
	18	11	100.0	11	24	AAK98619	Modified peptide n
	19	11	100.0	11	24	ABA97513	Peptide nucleic ac
	20	11	100.0	12	18	AAT89232	Peptide nucleic ac
	21	11	100.0	12	21	AAA37551	PNA sequence #8 us
	22	11	100.0	12	23	AAS15429	PNA V inhibiting h
	23	11	100.0	12	23	ABI05288	Oligonucleotide pr
c	24	11	100.0	12	23	ABI34202	Oligonucleotide pr
	25	11	100.0	13	18	AAT89225	Peptide nucleic ac
	26	11	100.0	13	18	AAT89236	Peptide nucleic ac
	27	11	100.0	13	21	AAA37544	PNA sequence #1 us
	28	11	100.0	13	21	AAA37555	PNA sequence #12 u
	29	11	100.0	13	22	AAF81195	Thiophosphoramidat
	30	11	100.0	13	23	AAS15423	PNA 8/VI inhibitin
	31	11	100.0	13	23	AAS15433	PNA 6/X inhibiting
	32	11	100.0	13	23	ABC19880	Oligonucleotide SE
c	33	11	100.0	13	23	ABC19881	Oligonucleotide SE
	34	11	100.0	13	23	ABF02802	Oligonucleotide SE
c	35	11	100.0	13	23	ABF02803	Oligonucleotide SE
	36	11	100.0	15	18	AAT89226	Peptide nucleic ac
	37	11	100.0	15	18	AAT89229	Peptide nucleic ac
c	38	11	100.0	15	18	AAT90068	Telomerase primer
	39	11	100.0	15	21	AAA37545	PNA sequence #2 us
	40	11	100.0	15	21	AAA37548	PNA sequence #5 us
	41	11	100.0	15	21	AAA37587	Antisense sequence
	42	11	100.0	15	23	AAS15424	PNA VII inhibiting
	43	11	100.0	15	23	AAS15427	PNA XIII inhibitin
	44	11	100.0	15	23	AAS15458	Phosphorothioate (
c	45	11	100.0	16	16	AAT01177	Telomeric repeat-b

ALIGNMENTS

RESULT 1
AAV07769
ID AAV07769 standard; DNA; 11 BP.
XX
AC AAV07769;
XX
DT 07-DEC-1998 (first entry)
XX
DE N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.
XX
KW telomerase inhibitor; phosphoramidate; telomerase-binding region; TBR;
KW cell proliferation; tumour; lukaemia; duplex; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..11
FT /*tag= a
FT /note= "each linkage is a phosphoramidate linkage"
XX
PN WO9737691-A1.
XX
PD 16-OCT-1997.
XX
PF 08-APR-1997; 97WO-US05773.
XX
PR 10-APR-1996; 96US-0630242.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Lloyd DH;
XX

```
DR   WPI; 1997-512422/47.
XX
PT   Treating elevated telomerase levels with N3 to P5 oligonucleotide
PT   phosphoramidates - that bind to the RNA component of telomerase,
PT   specifically for preventing growth of cancer cells, fungi and
PT   protozoa
XX
PS   Claim 5; Page 25; 38pp; English.
XX
CC   The invention relates to treatment of conditions associated with high
CC   levels of telomerase activity in a cell. The treatment comprises
CC   administering an oligonucleotide N3' => P5' phosphoramidate having a
CC   sequence complementary to part of the telomere-binding region (TBR) of
CC   the RNA component of telomerase, so as to inhibit its activity. The
CC   N3' => P5' oligonucleotide phosphoramidates are used therapeutically to
CC   inhibit cell proliferation, e.g. against a wide range of solid tumours
CC   or leukaemia, and also against fungal and protozoal pathogens. They are
CC   soluble and resistant to nuclease, and they bind strongly to RNA forming
CC   short but stable duplexes under physiological conditions. Thus they are
CC   very effective and selective inhibitors of telomerase. The present
CC   sequence represents a specific example of an oligonucleotide N3' => P5'
CC   phosphoramidate disclosed in the specification.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          1 GTTAGGGTTAG 11


RESULT 2
AAT89250/c
ID   AAT89250 standard; DNA; 11 BP.
XX
AC   AAT89250;
XX
DT   12-MAY-1998  (first entry)
XX
DE   DNA oligonucleotide 6, used in the measurement of Tm values.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; human telomerase RNA; hTR; PCR; oligonucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Example 2; Page 49; 76pp; English.
XX
CC   This is an oligonucleotide used in the measurement of Tm values and
CC   their complimentary peptide nucleic acids (PNAs), (e.g.
CC   AAT89231-T89240). PNAs hybridise specifically to an RNA component of
CC   mammalian telomerase, and include the sequence GGG for specific
CC   hybridisation to the template region of this component.  PNAs can be used
CC   as probes to detect the RNA component of mammalian telomerase and as
CC   inhibitors of telomerase activity, especially in the treatment of
CC   cancer.
XX
SQ   Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db         11 GTTAGGGTTAG 1


RESULT 3
AAT89237
ID   AAT89237 standard; DNA; 11 BP.
XX
AC   AAT89237;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Peptide nucleic acid 12, targeted to mammalian telomerase.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..13
FT                   /*tag=  a
FT                   /note= "Sugar-phosphate backbone has been replaced by
FT                          a peptide backbone"
FT   modified_base   1
FT                   /*tag=  b
FT                   /note= "Optionally conjugated to peptide AAW31919"
FT   modified_base   13
FT                   /*tag=  c
FT                   /note= "Optionally conjugated to peptide AAW31919"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Claim 9; Page 59; 76pp; English.
XX
CC   This sequence is a novel peptide nucleic acid (PNA), which acts as
CC   an inhibitor of mammalian, preferably human, telomerase.  The PNAs
CC   hybridise specifically to an RNA component of mammalian telomerase,
CC   and include the sequence GGG for specific hybridisation to the template
CC   region of this component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
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  Query Match            100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          1 GTTAGGGTTAG 11


RESULT 4
AAT90060
ID   AAT90060 standard; DNA; 11 BP.
XX
AC   AAT90060;
XX
DT   24-NOV-1997  (first entry)
XX
DE   Telomerase primer.
XX
KW   Detection; telomerase; amplification; polymerase chain reaction;
KW   PCR; primer; cancer; carcinoma; sarcoma; leukaemia; leukemia;
KW   myeloma; lymphoma; neuroblastoma; astrocytoma; glioma;
KW   glioblastoma; retinoblastoma; melanoma; screen; drug;
KW   determination; telomere length; ss.
XX
OS   Synthetic.
XX
PN   WO9711198-A1.
XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-US15162.
XX
PR   20-SEP-1995;   95US-0531743.
XX
PA   (CTRC-) CTRC RES FOUND.
XX
PI   Chen S,  Fletcher TM,  Maine I,  Qiu M,  Windle BE;
XX
DR   WPI; 1997-202904/18.
XX
PT   Detecting telomerase activity by ligation sequential reaction -
PT   useful for diagnosis of cancer or to screen for telomerase
PT   inhibitors
XX
PS   Claim 40; Page 27; 71pp; English.
XX
CC   A novel method of detecting telomerase activity in a sample,
CC   comprises amplifying a sample with a telomerase primer, e.g. the
CC   present sequence, and contacting the product with 1st and 2nd
CC   oligonucleotides, which hybridise to the product so that no single
CC   stranded region intervenes between them. The hybridised product and
CC   oligonucleotides are then contacted with ligase and the ligated
CC   form of the oligonucleotides detected.
CC   The method can be used to detect cancer, e.g. carcinomas of the
CC   breast, colon, oesophagus, kidney, liver, lung, ovaries, prostate,
CC   stomach, uterus, pancreas and head and neck, sarcomas of bone and
CC   muscle, leukaemias, myelomas, lymphomas, neuroblastomas,
CC   astrocytomas, gliomas, glioblastomas, retinoblastomas and
CC   melanomas. The method can also be used to screen for
CC   anti-telomerase activity in candidate drugs and to determine
CC   telomere length.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match            100.0%;  Score 11;  DB 18;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          1 GTTAGGGTTAG 11


RESULT 5
AAA37556
ID   AAA37556 standard; DNA; 11 BP.
XX
AC   AAA37556;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #13 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 6; Column 71; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
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CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 6
AAA37561
ID   AAA37561 standard; DNA; 11 BP.
XX
AC   AAA37561;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #18 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
FT   misc_feature    1
FT                   /*tag=  b
FT                   /note= "G residue is linked to the carboxy end of the
FT                          peptide GGRQIKIWFQNNMKWKK"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase
XX
PS   Claim 9; Column 71-72; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 7
AAA37562
ID   AAA37562 standard; DNA; 11 BP.
XX
AC   AAA37562;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #19 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
FT   misc_feature    11
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FT                          peptide GGRQIKIWFQNNMKWKK"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
```

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XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Claim 9; Column 71-72; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          1 GTTAGGGTTAG 11


RESULT 8
AAA37573/c
ID   AAA37573 standard; DNA; 11 BP.
XX
AC   AAA37573;
XX
DT   15-AUG-2000  (first entry)
XX
DE   PNA sequence #31 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag=  a
FT                   /note= "Peptide nucleic acid molecule, where
FT                          N-(2-aminoethyl)glycine units are linked to
FT                          nucleotide bases via glycine amino N through a
FT                          methylenecarbonyl linker"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Example 2; Column 33; 45pp; English.
XX
CC   The present sequence represents a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db         11 GTTAGGGTTAG 1


RESULT 9
AAA37586
ID   AAA37586 standard; DNA; 11 BP.
XX
AC   AAA37586;
XX
DT   15-AUG-2000  (first entry)
XX
```

```
DE   Antisense sequence #44 used to inhibit telomerase activity.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..11
FT                   /*tag= a
FT                   /note= "Phosphorothioate internucleotide linkages"
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-0838545.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT   activity in mammalian cells is useful as probes to detect the RNA
PT   component of a mammalian telomerase  -
XX
PS   Example 1; Column 27-28; 45pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide used as a
CC   control sequence alongside a peptide nucleic acid molecule which
CC   hybridises to the mRNA component of mammalian telomerase, and inhibits
CC   telomerase activity. Telomerase is a ribonucleoprotein enzyme that
CC   synthesizes one strand of the telomeric DNA, using as a template an 11
CC   nucleotide sequence contained within the RNA component of the enzyme. The
CC   invention relates to PNA molecules having a sequence of no more than 25
CC   bases, which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 21;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 10
AAF81185
ID   AAF81185 standard; DNA; 11 BP.
XX
AC   AAF81185;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Oligonucleotide thiophosphoramidate, SEQ ID NO: 1.
XX
KW   Thiophosphoramidate oligonucleotide; virucide; cytostatic;
KW   immunosuppressive; contraceptive; RNA inhibitor; telomerase inhibitor;
KW   antisense therapy; viral infection; cancer; hyperproliferative disorder;
KW   autoimmune disorder; ss.
XX
OS   Synthetic.
XX
PN   WO200118015-A1.
XX
PD   15-MAR-2001.
XX
PF   08-SEP-2000; 2000WO-US24688.
XX
PR   10-SEP-1999;   99US-0153201.
PR   19-OCT-1999;   99US-0160444.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Pongracz K,  Matray T;
XX
DR   WPI; 2001-265967/27.
XX
PT   Novel thiophosphoramidate polynucleotide useful for detection of RNA or
PT   DNA having a given target sequence, for inhibiting RNA function in a
PT   cell, and for treating cancer and viral infection  -
XX
PS   Example 3; Page 39; 68pp; English.
XX
CC   The present sequence was synthesised in an example illustrating an
CC   invention relating to polynucleotides comprising a non-homopolymeric
CC   sequence of nucleoside subunits joined by at least one inter-subunit
CC   linkage that is a N3'-P5' thiophosphoramidate. The thiophosphoramidate
CC   oligonucleotides retain a high RNA binding affinity and exhibit a much
CC   higher acid stability. They are useful for detecting a specific sequence
CC   in a sample, by forming a hybridisation complex with the sequence. They
CC   are useful for inhibiting function of an RNA in a cell (for inhibiting
CC   translation of a mRNA or for inhibiting telomerase enzyme in a cell).
CC   They are also useful in the preparation of a medicament for treatment of
CC   viral infection or cancer. The oligonucleotides are useful for anti-sense
CC   and anti-gene diagnostic or therapeutic applications and may be used for
CC   treating telomerase-mediated conditions or diseases, such as
CC   hyperproliferative and autoimmune disorders, and for contraceptive
CC   purposes.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 11
AAH26728
ID   AAH26728 standard; DNA; 11 BP.
XX
```

```
AC   AAH26728;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Phosphoramidate-linked 2'-arabino-fluorooligonucleotide.
XX
KW   2'-arabino-fluorooligonucleotide; phosphoramidate; telomerase;
KW   inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW   virucide; antisense; antigene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2..11
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "2'-arabino-fluoronucleosides"
FT   modified_base   2..11
FT                   /*tag=  b
FT                   /mod_base= "OTHER"
FT                   /note= "phosphoramidate linkage"
XX
PN   WO200153307-A1.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01918.
XX
PR   21-JAN-2000; 2000US-178248P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Schultz RG;
XX
DR   WPI; 2001-589652/66.
XX
PT   Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT   function of RNA and telomerase enzymes and to treat e.g. viral
PT   infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT   nucleoside(s) -
XX
PS   Example 6; Page 46; 61pp; English.
XX
CC   The present sequence is that of a N3'-P5' 2'-arabino-fluoro
CC   phosphoramidate oligonucleotide that is complementary to
CC   telomerase RNA.  The oligonucleotide was used to assess the
CC   relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC   oligonucleotides and their 2'-ribo fluorooligonucleotide
CC   counterparts (see AAH26728-35) for the inhibition of telomerase
CC   activity.  Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC   are generally more acid stable, more resistant to cellular
CC   proteases, and also show greater telomerase inhibition activity
CC   than 2'-ribose-fluoro phosphoramidates.  They are therefore useful
CC   for treating cancer (claimed) and other diseases in which telomerase
CC   activity is present at abnormal levels, such as hyperproliferative
CC   or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC   immune system disorders requiring immunosuppression, and in the
CC   treatment of viral infection (claimed).
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 12
AAH26732
ID   AAH26732 standard; DNA; 11 BP.
XX
AC   AAH26732;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Phosphoramidate-linked 2'-ribose-fluorooligonucleotide.
XX
KW   2'-ribose-fluorooligonucleotide; phosphoramidate; telomerase;
KW   inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
KW   virucide; antisense; antigene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2..11
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "2'-ribose-fluoronucleosides"
FT   modified_base   2..11
FT                   /*tag=  b
FT                   /mod_base= "OTHER"
FT                   /note= "phosphoramidate linkage"
XX
PN   WO200153307-A1.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US01918.
XX
PR   21-JAN-2000; 2000US-178248P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gryaznov S,  Schultz RG;
XX
DR   WPI; 2001-589652/66.
XX
PT   Polynucleotides, used to detect and isolate nucleic acids, inhibit
PT   function of RNA and telomerase enzymes and to treat e.g. viral
PT   infections, contain 2'-arabino-fluoronucleoside(s) linked to
PT   nucleoside(s) -
XX
PS   Example 6; Page 46; 61pp; English.
XX
CC   The present sequence is that of a 2'-ribose-fluoro
CC   phosphoramidate oligonucleotide that is complementary to
CC   telomerase RNA.  The oligonucleotide was used to assess the
CC   relative efficacy of novel 2'-arabino-fluoro phosphoramidate
CC   oligonucleotides and their 2'-ribose fluorooligonucleotide
CC   counterparts (see AAH26728-35) for the inhibition of telomerase
CC   activity.  Novel phosphoramidate 2'-arabino-fluorooligonucleotides
CC   are generally more acid stable, more resistant to cellular
CC   proteases, and also show greater telomerase inhibition activity
CC   than 2'-ribose-fluoro phosphoramidates.  They are therefore useful
CC   for treating cancer (claimed) and other diseases in which telomerase
CC   activity is present at abnormal levels, such as hyperproliferative
CC   or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
CC   immune system disorders requiring immunosuppression, and in the
CC   treatment of viral infection (claimed).
XX
SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 22;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 13
AAS14909
```

```
ID   AAS14909 standard; DNA; 11 BP.
XX
AC   AAS14909;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #5.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= g
FT                   /note= "Optionally phosphorylated"
FT   modified_base   1..11
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Optionally phosphorothiolate linkages"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #5, representative
CC   of the telomere over-hang sequence and one of the oligonucleotides used
CC   to inhibit mammalian epithelial cell proliferation, described in the
CC   method of the invention.
XX

SQ   Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 23;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          1 GTTAGGGTTAG 11


RESULT 14
AAS14913/c
ID   AAS14913 standard; DNA; 11 BP.
XX
AC   AAS14913;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #9.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= c
FT                   /note= "Phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Example 12; Page 37; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
```

CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #9, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC described in the method of the invention.
XX
SQ Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
||||||||||
Db 11 GTTAGGGTTAG 1

RESULT 15
AAS15434
ID AAS15434 standard; DNA; 11 BP.
XX
AC AAS15434;
XX
DT 14-FEB-2002 (first entry)
XX
DE PNA 7/IV inhibiting human and mammalian telomerase activity.
XX
KW Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW inflammation; lymphoproliferative disease; autoimmune disease;
KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immunodeficiency syndrome;
KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW immunosuppressive; polyamide backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..11
FT /*tag= a
FT /note= "This sequence is a peptide nucleic acid, i.e. it
FT contains a polyamide backbone instead of a
FT deoxyribose backbone"
XX
PN US6294650-B1.
XX
PD 25-SEP-2001.
XX
PF 08-JUL-1999; 99US-0349532.
XX
PR 09-APR-1997; 97US-0838545.
PR 09-APR-1996; 96US-0630019.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;
XX
DR WPI; 2001-638024/73.
XX
PT New peptide nucleic acids that hybridizes to the RNA component of
PT mammalian telomerase, useful for treating or preventing cancer,
PT inflammation, lymphoproliferative diseases, autoimmune disease, or
PT neurodegenerative diseases -
XX
PS Claim 7; Column 73; 46pp; English.
XX
CC The present invention relates to peptide nucleic acids (PNAs), comprising
CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC mammalian cells by hybridising to the RNA component of mammalian
CC telomerase. The PNAs are useful as probes to detect the RNA component
CC of mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase
CC RNA component (hTR) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents one of the PNA sequences
CC of the invention.
XX
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
||||||||||
Db 1 GTTAGGGTTAG 11

Search completed: June 2, 2003, 18:45:12
Job time : 183.98 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:29:55 ; Search time 1380.37 Seconds
(without alignments)
129.060 Million cell updates/sec

Title: US-09-540-843-5
Perfect score: 11
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	11	100.0	19	17	AZ614760	AZ614760 1M0443A17
c	2	11	100.0	20	17	TA158A03P	AL472050 T. brucei
	3	11	100.0	25	17	TA84A06P	AL462065 T. brucei
c	4	11	100.0	27	17	AZ803795	AZ803795 2M0064D22
c	5	11	100.0	40	17	AZ380089	AZ380089 1M0135K14
	6	9.4	85.5	22	17	AZ666649	AZ666649 1M0548M19
c	7	9.4	85.5	29	17	AZ514597	AZ514597 1M0361E14
	8	9.4	85.5	33	12	BG419809	BG419809 602453261
c	9	9.4	85.5	33	17	AZ334282	AZ334282 1M0063B08
c	10	9.4	85.5	34	17	AZ776073	AZ776073 2M0009M20
c	11	9.4	85.5	36	17	AL767851	AL767851 Arabidops
	12	9.4	85.5	39	9	AU008671	AU008671 AU008671
c	13	9	81.8	22	14	D18745	D18745 MUSGS01807
	14	9	81.8	31	17	AL756692	AL756692 Arabidops
c	15	9	81.8	32	9	AU255689	AU255689 AU255689
c	16	9	81.8	33	17	BH862417	BH862417 SALK_0898
c	17	9	81.8	34	17	AZ643251	AZ643251 1M0506F04
	18	9	81.8	36	17	BH789800	BH789800 SALK_0467
c	19	9	81.8	40	9	AI507758	AI507758 sb12c12.y
c	20	9	81.8	40	14	W12126	W12126 ma60g05.r1
	21	8.4	76.4	21	17	AZ766315	AZ766315 1M0563K14
c	22	8.4	76.4	23	17	TA319C11P	AL492458 T. brucei
c	23	8.4	76.4	24	9	AU256889	AU256889 AU256889
	24	8.4	76.4	25	10	AV544203	AV544203 AV544203
c	25	8.4	76.4	25	17	TA274G11Q	AL485967 T. brucei
c	26	8.4	76.4	27	9	AU255344	AU255344 AU255344
c	27	8.4	76.4	27	14	L32043	L32043 HUMXP2G6A H
	28	8.4	76.4	27	17	AZ789654	AZ789654 2M0037G08
	29	8.4	76.4	30	10	BE385567	BE385567 601275826
c	30	8.4	76.4	30	17	AZ761166	AZ761166 1M0555A21
	31	8.4	76.4	31	10	BE409249	BE409249 601301117
c	32	8.4	76.4	31	13	BM017239	BM017239 603643882
c	33	8.4	76.4	31	17	AZ782241	AZ782241 2M0022A21
	34	8.4	76.4	32	12	BE901763	BE901763 601675392
c	35	8.4	76.4	32	17	AZ803815	AZ803815 2M0064H19
c	36	8.4	76.4	32	17	AL766020	AL766020 Arabidops
c	37	8.4	76.4	33	17	AZ591773	AZ591773 1M0402M06
	38	8.4	76.4	34	9	AI047833	AI047833 ud64c05.x
	39	8.4	76.4	34	9	AI132658	AI132658 ue33b11.x
	40	8.4	76.4	34	12	BE729288	BE729288 601561653
c	41	8.4	76.4	34	13	BI913027	BI913027 603176563
c	42	8.4	76.4	34	17	TA293C07Q	AL485635 T. brucei
c	43	8.4	76.4	35	9	AU263853	AU263853 AU263853
c	44	8.4	76.4	35	17	AZ389531	AZ389531 1M0150P07
c	45	8.4	76.4	36	14	R77023	R77023 yi66d09.r1

ALIGNMENTS

RESULT 1
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LOCUS AZ614760 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, DNA sequence.
ACCESSION AZ614760
VERSION AZ614760.1 GI:11736950
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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            Plate: 0443  row: A  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="Mus musculus"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0443A17"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
BASE COUNT        3 a      0 c      10 g      6 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          3 GTTAGGGTTAG 13


RESULT 2
TA158A03P/c
LOCUS       TA158A03P                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 158a03, forward sequence,
            genomic survey sequence.
ACCESSION   AL472050
VERSION     AL472050.1  GI:11837404
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="Trypanosoma brucei"
                    /strain="TREU927"
                    /db_xref="taxon:5691"
                    /clone="158a03"
BASE COUNT        6 a      11 c      0 g      3 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 17;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         20 GTTAGGGTTAG 10


RESULT 3
TA84A06P
LOCUS       TA84A06P                  25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 84a06, forward sequence,
            genomic survey sequence.
ACCESSION   AL462065
VERSION     AL462065.1  GI:11860923
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES            Location/Qualifiers
     source         1. .25
                    /organism="Trypanosoma brucei"
                    /strain="TREU927"
                    /db_xref="taxon:5691"
                    /clone="84a06"
BASE COUNT        4 a      0 c      12 g      9 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          6 GTTAGGGTTAG 16
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```
RESULT 4
AZ803795/c
LOCUS       AZ803795                  27 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0064D22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0064D22 F, DNA sequence.
ACCESSION   AZ803795
VERSION     AZ803795.1  GI:12956118
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0064  row: D  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0064D22"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        9 a     11 c      2 g      5 t
ORIGIN

  Query Match           100.0%;  Score 11;  DB 17;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 7.9e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         26 GTTAGGGTTAG 16
```

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RESULT 5
AZ380089/c
LOCUS       AZ380089                  40 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0135K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0135K14 R, DNA sequence.
ACCESSION   AZ380089
VERSION     AZ380089.1  GI:10493789
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0135  row: K  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0135K14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       14 a     15 c      1 g     10 t
ORIGIN

  Query Match           100.0%;  Score 11;  DB 17;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 8.9e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         12 GTTAGGGTTAG 2
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RESULT 6
AZ666649
LOCUS AZ666649 22 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0548M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0548M19 R, DNA sequence.
ACCESSION AZ666649
VERSION AZ666649.1 GI:11803795
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: M column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0548M19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 14 g 5 t
ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 22;
Best Local Similarity 90.9%; Pred. No. 6.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
||||||| |||
Db 4 GTTAGGGGTAG 14

RESULT 7
AZ514597/c
LOCUS AZ514597 29 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0361E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361E14 F, DNA sequence.
ACCESSION AZ514597
VERSION AZ514597.1 GI:10695829
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: E column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361E14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 9 c 6 g 8 t
ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 29;
Best Local Similarity 90.9%; Pred. No. 7.5e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
|| |||||||||
Db 12 GTAAGGGTTAG 2

```
RESULT 8
BG419809
LOCUS       BG419809                 33 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602453261F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4591599 5',
            mRNA sequence.
ACCESSION   BG419809
VERSION     BG419809.1  GI:13326315
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1328  row: j  column: 16
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4591599"
                     /clone_lib="NIH_MGC_14"
                     /tissue_type="renal cell adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        9 a      3 c     12 g      9 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 12;  Length 33;
  Best Local Similarity   90.9%;  Pred. No. 7.8e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              |||||||| ||
Db          7 GTTAGGGTGAG 17


RESULT 9
AZ334282/c
LOCUS       AZ334282                 33 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0063B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0063B08 R, DNA sequence.
ACCESSION   AZ334282
VERSION     AZ334282.1  GI:10401456
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0063  row: B  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0063B08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a     13 c      2 g      7 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 17;  Length 33;
  Best Local Similarity   90.9%;  Pred. No. 7.8e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||| |||||||
Db         22 GTTGGGGTTAG 12


RESULT 10
AZ776073/c
LOCUS       AZ776073                 34 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0009M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0009M20 F, DNA sequence.
ACCESSION   AZ776073
VERSION     AZ776073.1  GI:12903271
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: M column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
FEATURES Location/Qualifiers
source 1. .34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0009M20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 19 a 9 c 2 g 4 t
ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 34;
Best Local Similarity 90.9%; Pred. No. 7.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
||||| |||||
Db 20 GTTAGAGTTAG 10

RESULT 11
AL767851/c
LOCUS AL767851 36 bp DNA linear GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-222E01-014236, genomic survey sequence.
ACCESSION AL767851
VERSION AL767851.1 GI:21520970
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 36)
AUTHORS Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F28H19. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .36
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-222E01-014236"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
BASE COUNT 14 a 10 c 4 g 8 t
ORIGIN

Query Match 85.5%; Score 9.4; DB 17; Length 36;
Best Local Similarity 90.9%; Pred. No. 8e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
| |||||||||
Db 24 GATAGGGTTAG 14

RESULT 12
AU008671
LOCUS AU008671 39 bp mRNA linear EST 31-JUL-1998
DEFINITION AU008671 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc03845, mRNA sequence.
ACCESSION AU008671
VERSION AU008671.1 GI:3345129
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 39)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
source 1. .39
/organism="Schizosaccharomyces pombe"

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                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc03845"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /sex="h minus"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
BASE COUNT       11 a      3 c     12 g     13 t
ORIGIN

  Query Match             85.5%;  Score 9.4;  DB 9;  Length 39;
  Best Local Similarity   90.9%;  Pred. No. 8.2e+04;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              | |||||||||
Db         24 GCTAGGGTTAG 34


RESULT 13
D18745/c
LOCUS       D18745                    22 bp    mRNA    linear   EST 12-DEC-1995
DEFINITION  MUSGS01807 Mouse 3'-directed Mus musculus domesticus cDNA clone
            md1403 3', mRNA sequence.
ACCESSION   D18745
VERSION     D18745.1  GI:1100714
KEYWORDS    EST.
SOURCE      western European house mouse.
  ORGANISM  Mus musculus domesticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
  TITLE     Analysis of gene expression in mouse embryogenesis by 3'-directed
            cDNA sequencing
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara
            ,K.
            Institute for Cellular and Molecular Biology
            Osaka University
            3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus domesticus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10092"
                     /clone="md1403"
                     /clone_lib="Mouse 3'-directed"
                     /tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
BASE COUNT       7 a      5 c      1 g      9 t
ORIGIN

  Query Match             81.8%;  Score 9;  DB 14;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TTAGGGTTA 10
              |||||||||
Db         21 TTAGGGTTA 13


RESULT 14
AL756692
LOCUS       AL756692                  31 bp    DNA     linear   GSS 17-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331,
            genomic survey sequence.
ACCESSION   AL756692
VERSION     AL756692.1  GI:21489190
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 31)
  AUTHORS   Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the right border of the T-DNA. It
            indicates an insertion close to or within gene At1g17190. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-111H11-012331"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT       8 a      0 c     10 g     13 t
ORIGIN

  Query Match             81.8%;  Score 9;  DB 17;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTT 9
              |||||||||
Db         10 GTTAGGGTT 18


RESULT 15
AU255689/c
LOCUS       AU255689                  32 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU255689 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0006171 3', mRNA sequence.
ACCESSION   AU255689
VERSION     AU255689.1  GI:20318670
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
```

```
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="BED0006171"
                     /clone_lib="3'-directed mouse cDNA library"
                     /tissue_type="brain"
                     /note="Vector: pGEM-T-easy"
BASE COUNT       10 a      8 c      6 g      8 t
ORIGIN

  Query Match             81.8%;  Score 9;  DB 9;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TTAGGGTTA 10
              |||||||||
Db         31 TTAGGGTTA 23


Search completed: June  2, 2003, 20:35:47
Job time : 1384.37 secs
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:31:20 ; Search time 45.0732 Seconds
(without alignments)
74.844 Million cell updates/sec

Title: US-09-540-843-5
Perfect score: 11
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	11	100.0	11	1	US-08-330-123A-2	Sequence 2, Appli
c	2	11	100.0	11	1	US-08-482-115B-2	Sequence 2, Appli
c	3	11	100.0	11	2	US-08-660-678A-2	Sequence 2, Appli
	4	11	100.0	11	2	US-08-531-743-11	Sequence 11, Appl
c	5	11	100.0	11	2	US-08-531-743-12	Sequence 12, Appl
c	6	11	100.0	11	2	US-08-485-778-36	Sequence 36, Appl
c	7	11	100.0	11	2	US-08-472-802C-3	Sequence 3, Appli
c	8	11	100.0	11	3	US-08-520-550A-36	Sequence 36, Appl
	9	11	100.0	11	3	US-08-630-019A-9	Sequence 9, Appli
c	10	11	100.0	11	3	US-08-630-019A-30	Sequence 30, Appl
	11	11	100.0	11	3	US-08-630-019A-39	Sequence 39, Appl
	12	11	100.0	11	3	US-08-838-545-13	Sequence 13, Appl
c	13	11	100.0	11	3	US-08-838-545-31	Sequence 31, Appl
	14	11	100.0	11	3	US-08-838-545-44	Sequence 44, Appl
c	15	11	100.0	11	3	US-08-998-443-2	Sequence 2, Appli
c	16	11	100.0	11	4	US-09-060-523-2	Sequence 2, Appli
	17	11	100.0	11	4	US-09-349-532-13	Sequence 13, Appl
c	18	11	100.0	11	4	US-09-349-532-31	Sequence 31, Appl
	19	11	100.0	11	4	US-09-349-532-44	Sequence 44, Appl
c	20	11	100.0	11	4	US-09-580-517-2	Sequence 2, Appli
	21	11	100.0	12	3	US-08-630-019A-10	Sequence 10, Appl
	22	11	100.0	12	3	US-08-838-545-8	Sequence 8, Appli
	23	11	100.0	12	4	US-09-349-532-8	Sequence 8, Appli
	24	11	100.0	13	3	US-08-630-019A-11	Sequence 11, Appl
	25	11	100.0	13	3	US-08-630-019A-15	Sequence 15, Appl
	26	11	100.0	13	3	US-08-838-545-1	Sequence 1, Appli
	27	11	100.0	13	3	US-08-838-545-12	Sequence 12, Appl
	28	11	100.0	13	4	US-09-349-532-1	Sequence 1, Appli
	29	11	100.0	13	4	US-09-349-532-12	Sequence 12, Appl
c	30	11	100.0	15	2	US-08-531-743-4	Sequence 4, Appli
	31	11	100.0	15	3	US-08-630-019A-12	Sequence 12, Appl
	32	11	100.0	15	3	US-08-630-019A-18	Sequence 18, Appl
	33	11	100.0	15	3	US-08-630-019A-40	Sequence 40, Appl
	34	11	100.0	15	3	US-08-838-545-2	Sequence 2, Appli
	35	11	100.0	15	3	US-08-838-545-5	Sequence 5, Appli
	36	11	100.0	15	3	US-08-838-545-45	Sequence 45, Appl
	37	11	100.0	15	4	US-09-349-532-2	Sequence 2, Appli
	38	11	100.0	15	4	US-09-349-532-5	Sequence 5, Appli
	39	11	100.0	15	4	US-09-349-532-45	Sequence 45, Appl
c	40	11	100.0	16	1	US-08-153-051B-11	Sequence 11, Appl
c	41	11	100.0	16	2	US-08-151-477A-11	Sequence 11, Appl
c	42	11	100.0	16	3	US-08-819-867-20	Sequence 20, Appl
c	43	11	100.0	16	4	US-08-464-011B-60	Sequence 60, Appl
	44	11	100.0	17	2	US-08-531-743-13	Sequence 13, Appl
c	45	11	100.0	17	4	US-08-857-721-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-08-330-123A-2/c
; Sequence 2, Application US/08330123A
; Patent No. 5583016
;  GENERAL INFORMATION:
;    APPLICANT:  VILLEPONTEAU, Bryant
;    APPLICANT:  FENG, Junli
;    APPLICANT:  FUNK, Walter
;    APPLICANT:  ANDREWS, William H.
;    TITLE OF INVENTION:  HUMAN TELOMERASE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,123A
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000810
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-330-123A-2

  Query Match           100.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GTTAGGGTTAG 11
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Db         11 GTTAGGGTTAG 1


RESULT 2
US-08-482-115B-2/c
; Sequence 2, Application US/08482115B
; Patent No. 5776679
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Assays for the RNA Component of Human
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,115B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000830US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-482-115B-2

  Query Match             100.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 3
US-08-660-678A-2/c
; Sequence 2, Application US/08660678A
; Patent No. 5837857
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678A
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-660-678A-2

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 4
US-08-531-743-11
; Sequence 11, Application US/08531743
; Patent No. 5856096
;  GENERAL INFORMATION:
;    APPLICANT:  Windle, Bradford E.
;    APPLICANT:  Qiu, Ming
;    APPLICANT:  Chen, Shi-fong
;    APPLICANT:  Fletcher, Terace M.
;    APPLICANT:  Maine, Ira
;    TITLE OF INVENTION:  Rapid and Sensitive Assays for Detecting and
;    TITLE OF INVENTION:  Distinguishing Between Processive and
;    TITLE OF INVENTION:  No. 5856096-Processive Telomerase Activities
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/531,743
;       FILING DATE:  20-SEP-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Highlander, Steven L.
;       REGISTRATION NUMBER:  37,642
;       REFERENCE/DOCKET NUMBER:  CTRC:026/HYL
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-531-743-11

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          1 GTTAGGGTTAG 11


RESULT 5
US-08-531-743-12/c
; Sequence 12, Application US/08531743
; Patent No. 5856096
;  GENERAL INFORMATION:
;    APPLICANT:  Windle, Bradford E.
;    APPLICANT:  Qiu, Ming
;    APPLICANT:  Chen, Shi-fong
;    APPLICANT:  Fletcher, Terace M.
;    APPLICANT:  Maine, Ira
;    TITLE OF INVENTION:  Rapid and Sensitive Assays for Detecting and
;    TITLE OF INVENTION:  Distinguishing Between Processive and
;    TITLE OF INVENTION:  No. 5856096-Processive Telomerase Activities
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/531,743
;      FILING DATE:  20-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  CTRC:026/HYL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-531-743-12

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 6
US-08-485-778-36/c
; Sequence 36, Application US/08485778
; Patent No. 5876979
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel Athena
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria Antonia Blasco
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA COMPONENT OF TELOMERASE
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,778
;      FILING DATE:  07-JE-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-485-778-36

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1
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RESULT 7
US-08-472-802C-3/c
; Sequence 3, Application US/08472802C
; Patent No. 5958680
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,802C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000820
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-472-802C-3

  Query Match             100.0%;  Score 11;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 8
US-08-520-550A-36/c
; Sequence 36, Application US/08520550A
; Patent No. 6013468
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel A.
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria A. B.
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA Component of Telomerase
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/520,550A
;      FILING DATE:  29-AUG-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A3B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-520-550A-36

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 9
US-08-630-019A-9
; Sequence 9, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/630,019A
;       FILING DATE:  09-JUN-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Storella, John R.
;       REGISTRATION NUMBER:  32,944
;       REFERENCE/DOCKET NUMBER:  015389-001600US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;       DESCRIPTION:  where (deoxy)ribose-phosphate linkages are replaced by
;       DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;       DESCRIPTION:  glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-9

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 10
US-08-630-019A-30/c
; Sequence 30, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-630-019A-30

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db         11 GTTAGGGTTAG 1


RESULT 11
US-08-630-019A-39
; Sequence 39, Application US/08630019A
; Patent No. 6015710
;  GENERAL INFORMATION:
;    APPLICANT:  Shay, Jerry W.
;    APPLICANT:  Wright, Woodring E.
;    APPLICANT:  Piatyszek, Mieczyslaw A.
;    APPLICANT:  Corey, David
;    APPLICANT:  No. 6015710ton, James C.
;    TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;    TITLE OF INVENTION:  Peptide Nucleic Acids
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,019A
;      FILING DATE:  09-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001600US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "phosphorothioate (PS) nucleic acid"
US-08-630-019A-39

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 12
US-08-838-545-13
; Sequence 13, Application US/08838545
; Patent No. 6046307
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; GENERAL INFORMATION:
;   APPLICANT:  Shay, Jerry W.
;   APPLICANT:  Wright, Woodring E.
;   APPLICANT:  Piatyszek, Mieczyslaw A.
;   APPLICANT:  Corey, David R.
;   APPLICANT:  No. 6046307ton, James C.
;   TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;   TITLE OF INVENTION:  Peptide Nucleic Acids
;   NUMBER OF SEQUENCES:  60
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP
;     STREET:  Two Embarcadero Center, Eighth Floor
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/838,545
;     FILING DATE:  09-APR-1997
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/630,019
;     FILING DATE:  09-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Storella, John R.
;     REGISTRATION NUMBER:  32,944
;     REFERENCE/DOCKET NUMBER:  015389-001610US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 576-0200
;     TELEFAX:  (415) 576-0300
; INFORMATION FOR SEQ ID NO:  13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  other nucleic acid
;     DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;     DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;     DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;     DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-13

  Query Match           100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 13
US-08-838-545-31/c
; Sequence 31, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
;   APPLICANT:  Shay, Jerry W.
;   APPLICANT:  Wright, Woodring E.
;   APPLICANT:  Piatyszek, Mieczyslaw A.
;   APPLICANT:  Corey, David R.
;   APPLICANT:  No. 6046307ton, James C.
;   TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;   TITLE OF INVENTION:  Peptide Nucleic Acids
;   NUMBER OF SEQUENCES:  60
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP
;     STREET:  Two Embarcadero Center, Eighth Floor
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/838,545
;     FILING DATE:  09-APR-1997
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/630,019
;     FILING DATE:  09-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Storella, John R.
;     REGISTRATION NUMBER:  32,944
;     REFERENCE/DOCKET NUMBER:  015389-001610US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 576-0200
;     TELEFAX:  (415) 576-0300
; INFORMATION FOR SEQ ID NO:  31:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  other nucleic acid
;     DESCRIPTION:  /desc = "peptide nucleic acid (PNA),
;     DESCRIPTION:  where (deoxy(ribose-phosphate linkages are replaced by
;     DESCRIPTION:  N-(2-aminoethyl)glycine units linked to nucleotide bases via
;     DESCRIPTION:  glycine amino N through a methylenecarbonyl linker"
US-08-838-545-31

  Query Match           100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db         11 GTTAGGGTTAG 1


RESULT 14
US-08-838-545-44
; Sequence 44, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
;   APPLICANT:  Shay, Jerry W.
;   APPLICANT:  Wright, Woodring E.
;   APPLICANT:  Piatyszek, Mieczyslaw A.
;   APPLICANT:  Corey, David R.
;   APPLICANT:  No. 6046307ton, James C.
;   TITLE OF INVENTION:  Modulation of Mammalian Telomerase by
;   TITLE OF INVENTION:  Peptide Nucleic Acids
;   NUMBER OF SEQUENCES:  60
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP
;     STREET:  Two Embarcadero Center, Eighth Floor
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/838,545
;     FILING DATE:  09-APR-1997
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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,019
;      FILING DATE:  09-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001610US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "phosphorothioate (PS)
;      DESCRIPTION:  nucleic acid"
US-08-838-545-44

  Query Match             100.0%;  Score 11;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 15
US-08-998-443-2/c
; Sequence 2, Application US/08998443
; Patent No. 6054575
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,443
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678
;      FILING DATE:  05-JUN-1996
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-998-443-2

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  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db         11 GTTAGGGTTAG 1


Search completed: June  2, 2003, 20:38:35
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 19:09:45 ; Search time 78.0732 Seconds
(without alignments)
189.976 Million cell updates/sec

Title: US-09-540-843-5
Perfect score: 11
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 477662

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	100.0	11	9	US-09-835-370-63	Sequence 63, Appl
2	11	100.0	11	9	US-10-122-630-5	Sequence 5, Appli
c 3	11	100.0	11	9	US-10-122-630-9	Sequence 9, Appli
4	11	100.0	11	9	US-10-122-633-5	Sequence 5, Appli
c 5	11	100.0	11	9	US-10-122-633-9	Sequence 9, Appli
c 6	11	100.0	11	10	US-09-057-351-2	Sequence 2, Appli
7	11	100.0	13	9	US-09-893-252-4	Sequence 4, Appli
8	11	100.0	13	9	US-10-038-335-1	Sequence 1, Appli
9	11	100.0	13	9	US-10-038-335-2	Sequence 2, Appli
c 10	11	100.0	18	8	US-08-463-404-4	Sequence 4, Appli
11	11	100.0	18	8	US-08-463-404-5	Sequence 5, Appli
12	11	100.0	18	9	US-09-893-252-1	Sequence 1, Appli
c 13	11	100.0	18	9	US-10-132-002-2	Sequence 2, Appli
14	11	100.0	18	9	US-10-132-002-4	Sequence 4, Appli
c 15	11	100.0	18	9	US-10-238-732-2	Sequence 2, Appli
16	11	100.0	18	9	US-10-044-692-295	Sequence 295, App
17	11	100.0	18	9	US-10-044-692-296	Sequence 296, App
18	11	100.0	18	10	US-09-057-351-26	Sequence 26, Appl
c 19	11	100.0	18	10	US-09-947-659-1	Sequence 1, Appli
20	11	100.0	18	10	US-09-947-659-2	Sequence 2, Appli
21	11	100.0	18	10	US-09-947-659-7	Sequence 7, Appli
22	11	100.0	19	10	US-09-817-387-19	Sequence 19, Appl
23	11	100.0	20	9	US-09-888-326-808	Sequence 808, App
24	11	100.0	20	9	US-10-112-653-824	Sequence 824, App
25	11	100.0	20	9	US-10-017-995-853	Sequence 853, App
26	11	100.0	20	9	US-09-776-479-853	Sequence 853, App
27	11	100.0	20	10	US-09-057-351-40	Sequence 40, Appl
28	11	100.0	20	10	US-09-816-248-36	Sequence 36, Appl
29	11	100.0	20	10	US-09-816-248-37	Sequence 37, Appl
30	11	100.0	21	9	US-10-079-500B-1	Sequence 1, Appli
31	11	100.0	21	9	US-10-040-370A-1	Sequence 1, Appli
32	11	100.0	21	10	US-09-817-387-23	Sequence 23, Appl
33	11	100.0	21	10	US-09-817-387-28	Sequence 28, Appl
c 34	11	100.0	21	10	US-09-801-346-2	Sequence 2, Appli
35	11	100.0	21	10	US-09-923-541-1	Sequence 1, Appli
36	11	100.0	22	9	US-09-940-173A-2	Sequence 2, Appli
37	11	100.0	22	9	US-09-940-173A-8	Sequence 8, Appli
38	11	100.0	22	10	US-09-057-351-41	Sequence 41, Appl
39	11	100.0	22	10	US-09-730-893-2	Sequence 2, Appli
40	11	100.0	22	10	US-09-730-893-8	Sequence 8, Appli
41	11	100.0	23	10	US-09-817-387-14	Sequence 14, Appl
42	11	100.0	23	10	US-09-817-387-16	Sequence 16, Appl
43	11	100.0	23	10	US-09-817-387-18	Sequence 18, Appl
c 44	11	100.0	24	8	US-08-463-404-6	Sequence 6, Appli
45	11	100.0	24	8	US-08-463-404-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-835-370-63
; Sequence 63, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of PNA derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-63

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
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Db 1 GTTAGGGTTAG 11

RESULT 2
US-10-122-630-5
; Sequence 5, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina

```
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-5

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 3
US-10-122-630-9/c
; Sequence 9, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-9

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
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Db         11 GTTAGGGTTAG 1


RESULT 4
US-10-122-633-5
; Sequence 5, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-5

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db          1 GTTAGGGTTAG 11


RESULT 5
US-10-122-633-9/c
; Sequence 9, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-9

  Query Match             100.0%;  Score 11;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| |
Db         11 GTTAGGGTTAG 1
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```
RESULT 6
US-09-057-351-2/c
; Sequence 2, Application US/09057351
; Patent No. US20010034439A1
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,351
;      FILING DATE:  08-APR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000821US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-09-057-351-2

  Query Match             100.0%;  Score 11;  DB 10;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db         11 GTTAGGGTTAG 1


RESULT 7
US-09-893-252-4
; Sequence 4, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
;  APPLICANT: Styczynski, Peter
;  APPLICANT:  Ahluwalia, Gurpreet S.
;  TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
;  FILE REFERENCE: 00216-552001
;  CURRENT APPLICATION NUMBER: US/09/893,252
;  CURRENT FILING DATE:  2001-10-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 13
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-893-252-4

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   63.6%;  Pred. No. 2.2e+03;
  Matches    7;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              |::||||::|| 
Db          3 GUUAGGGUUAG 13


RESULT 8
US-10-038-335-1
; Sequence 1, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Hanecak, Ronnie
;  APPLICANT:  Brown-Driver, Vickie
;  APPLICANT:  Vickers, Timothy
;  APPLICANT:  Chiang, Ming-yi
;  APPLICANT:  Anderson, Kevin
;  TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-C
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: ISIS-4976
;  CURRENT APPLICATION NUMBER: US/10/038,335
;  CURRENT FILING DATE:  2001-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: No. US20030096776A1el sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense sequence
US-10-038-335-1

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   63.6%;  Pred. No. 2.2e+03;
  Matches    7;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              |::||||::|| 
Db          3 GUUAGGGUUAG 13


RESULT 9
US-10-038-335-2
; Sequence 2, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Hanecak, Ronnie
;  APPLICANT:  Brown-Driver, Vickie
```

```
;  APPLICANT:  Vickers, Timothy
;  APPLICANT:  Chiang, Ming-yi
;  APPLICANT:  Anderson, Kevin
;  TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Core
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: ISIS-4976
;  CURRENT APPLICATION NUMBER: US/10/038,335
;  CURRENT FILING DATE:  2001-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: No. US20030096776A1el sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense sequence
US-10-038-335-2

  Query Match             100.0%;  Score 11;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          3 GTTAGGGTTAG 13


RESULT 10
US-08-463-404-4/c
; Sequence 4, Application US/08463404
; Patent No. US20020127634A1
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,404
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/060,952
;      FILING DATE:  May 13, 1993
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-404-4

  Query Match             100.0%;  Score 11;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3


RESULT 11
US-08-463-404-5
; Sequence 5, Application US/08463404
; Patent No. US20020127634A1
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,404
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/060,952
;      FILING DATE:  May 13, 1993
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-404-5

  Query Match             100.0%;  Score 11;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          6 GTTAGGGTTAG 16


RESULT 12
US-09-893-252-1
; Sequence 1, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
;  APPLICANT: Styczynski, Peter
;  APPLICANT:  Ahluwalia, Gurpreet S.
;  TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
;  FILE REFERENCE: 00216-552001
;  CURRENT APPLICATION NUMBER: US/09/893,252
;  CURRENT FILING DATE:  2001-10-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-893-252-1

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          6 GTTAGGGTTAG 16


RESULT 13
US-10-132-002-2/c
; Sequence 2, Application US/10132002
; Publication No. US20030022204A1
;   GENERAL INFORMATION:
;        APPLICANT: Lansdorp, Peter
;        TITLE OF INVENTION: Method for Detecting Multiple Copies of
;                            a Repeat Sequence in a Nucleic Acid Molecule
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HOWSON & HOWSON
;             STREET: 321 No. US20030022204A1ristown Road
;             CITY: Spring House
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/132,002
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/730,635
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: B&P7USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 540-9200
;             TELEFAX: (215) 540-5818
;             TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-132-002-2

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3


RESULT 14
US-10-132-002-4
; Sequence 4, Application US/10132002
; Publication No. US20030022204A1
;   GENERAL INFORMATION:
;        APPLICANT: Lansdorp, Peter
;        TITLE OF INVENTION: Method for Detecting Multiple Copies of
;                            a Repeat Sequence in a Nucleic Acid Molecule
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HOWSON & HOWSON
;             STREET: 321 No. US20030022204A1ristown Road
;             CITY: Spring House
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/132,002
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/730,635
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: B&P7USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 540-9200
;             TELEFAX: (215) 540-5818
;             TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-132-002-4

  Query Match             100.0%;  Score 11;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db          6 GTTAGGGTTAG 16
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RESULT 15
US-10-238-732-2/c
; Sequence 2, Application US/10238732
; Publication No. US20030077635A1
; GENERAL INFORMATION:
; APPLICANT: DAKO A/S
; TITLE OF INVENTION: DENDRIMERS AND METHODS FOR THEIR PREPARATION AND USE
; FILE REFERENCE: P65587US1
; CURRENT APPLICATION NUMBER: US/10/238,732
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 09/606,315
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: PA 1999 00934
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: linker sequence.
US-10-238-732-2

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTAGGGTTAG 11
              ||||||||||| 
Db         16 GTTAGGGTTAG 6
```

Search completed: June 2, 2003, 23:43:14
Job time : 79.0732 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:06:10 ; Search time 247.39 Seconds
(without alignments)
823.475 Million cell updates/sec

Title: US-09-540-843-3
Perfect score: 7
Sequence: 1 agtatga 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		7	100.0	7	6	AX268755	AX268755 Sequence
2		7	100.0	7	6	AX268759	AX268759 Sequence
3		7	100.0	9	6	AX268753	AX268753 Sequence
4	c	7	100.0	10	6	AX377258	AX377258 Sequence
5		7	100.0	10	6	BD007857	BD007857 LPS activ
6		7	100.0	11	6	AX470905	AX470905 Sequence
7	c	7	100.0	12	6	A91497	A91497 Sequence 24
8	c	7	100.0	13	6	AX018746	AX018746 Sequence
9		7	100.0	14	6	A33152	A33152 Synthetic H
10		7	100.0	14	6	AR082813	AR082813 Sequence
11	c	7	100.0	14	6	AR088823	AR088823 Sequence
12	c	7	100.0	14	6	AX018748	AX018748 Sequence
13	c	7	100.0	14	6	AX343036	AX343036 Sequence
14		7	100.0	15	6	A33153	A33153 Synthetic H
15	c	7	100.0	15	6	AR041154	AR041154 Sequence
16		7	100.0	15	6	AR082814	AR082814 Sequence
17	c	7	100.0	15	6	AR130719	AR130719 Sequence
18	c	7	100.0	15	6	AR130720	AR130720 Sequence
19		7	100.0	15	6	AR131705	AR131705 Sequence
20		7	100.0	15	6	AR132890	AR132890 Sequence
21	c	7	100.0	15	6	AX018750	AX018750 Sequence
22	c	7	100.0	15	6	AX377250	AX377250 Sequence
23		7	100.0	15	6	I77317	I77317 Sequence 24
24		7	100.0	15	6	I77620	I77620 Sequence 32
25		7	100.0	16	6	AR002583	AR002583 Sequence
26	c	7	100.0	16	6	AR072256	AR072256 Sequence
27		7	100.0	16	6	AR105728	AR105728 Sequence
28	c	7	100.0	16	6	I26367	I26367 Sequence 59
29		7	100.0	17	6	A26687	A26687 Sonde Lip8.
30	c	7	100.0	17	6	AR032060	AR032060 Sequence
31	c	7	100.0	17	6	AR039517	AR039517 Sequence
32	c	7	100.0	17	6	AR039519	AR039519 Sequence
33	c	7	100.0	17	6	AR039521	AR039521 Sequence
34	c	7	100.0	17	6	AR039523	AR039523 Sequence
35	c	7	100.0	17	6	AR039965	AR039965 Sequence
36	c	7	100.0	17	6	AR039967	AR039967 Sequence
37	c	7	100.0	17	6	AR060343	AR060343 Sequence
38		7	100.0	17	6	AR082789	AR082789 Sequence
39		7	100.0	17	6	AX263248	AX263248 Sequence
40	c	7	100.0	17	6	AX263249	AX263249 Sequence
41		7	100.0	17	6	AX324985	AX324985 Sequence
42	c	7	100.0	17	6	AX324986	AX324986 Sequence
43		7	100.0	17	6	AX457048	AX457048 Sequence
44	c	7	100.0	17	6	AX457049	AX457049 Sequence
45		7	100.0	17	6	I37448	I37448 Sequence 46

ALIGNMENTS

RESULT 1
AX268755
LOCUS AX268755 7 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 3 from Patent WO0174342.
ACCESSION AX268755
VERSION AX268755.1 GI:16541827
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 3 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

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FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+09;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 2
AX268759
LOCUS       AX268759                  7 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 7 from Patent WO0174342.
ACCESSION   AX268759
VERSION     AX268759.1  GI:16541831
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 7 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+09;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 3
AX268753
LOCUS       AX268753                  9 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1 from Patent WO0174342.
ACCESSION   AX268753
VERSION     AX268753.1  GI:16541825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 1 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      4 g      2 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+09;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8


RESULT 4
AX377258/c
LOCUS       AX377258                 10 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 20 from Patent WO0212562.
ACCESSION   AX377258
VERSION     AX377258.1  GI:19573546
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kazemi,A., Kliem,S.E. and Koshy,B.
  TITLE     Haplotypes of the pla2g1b gene
  JOURNAL   Patent: WO 0212562-A 20 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      0 g      4 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 3


RESULT 5
BD007857
LOCUS       BD007857                 10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007857
VERSION     BD007857.1  GI:18636230
KEYWORDS    JP 2001069993-A/133.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 133 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/133
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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BASE COUNT        4 a      0 c      4 g      2 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 6
AX470905
LOCUS       AX470905                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 482 from Patent WO02053773.
ACCESSION   AX470905
VERSION     AX470905.1  GI:22206030
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 482 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      2 c      2 g      3 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 7
A91497/c
LOCUS       A91497                    12 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 24 from Patent WO9824928.
ACCESSION   A91497
VERSION     A91497.1  GI:6740452
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Pallisgaard,N. and Hokland,P.
  TITLE     DETECTION OF CHROMOSOMAL ABNORMALITIES
  JOURNAL   Patent: WO 9824928-A 24 11-JUN-1998;
            PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      2 g      4 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 6.9e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         11 AGTATGA 5


RESULT 8
AX018746/c
LOCUS       AX018746                  13 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9943848.
ACCESSION   AX018746
VERSION     AX018746.1  GI:10042869
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Ong,C.J. and Jirik,F.R.
  TITLE     Protein interaction and transcription factor trap
  JOURNAL   Patent: WO 9943848-A 4 02-SEP-1999;
            ONG CHRISTOPHER J (CA); UNIV BRITISH COLUMBIA (CA); JIRIK FRANK R
            (CA)
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligomer for adjusting a reading frame for
                     ligation"
BASE COUNT        3 a      4 c      1 g      5 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 6.8e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          7 AGTATGA 1


RESULT 9
A33152
LOCUS       A33152                    14 bp    DNA     linear   PAT 07-MAY-1996
DEFINITION  Synthetic HLA DR typing probe.
ACCESSION   A33152
VERSION     A33152.1  GI:1567736
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      1 c      4 g      3 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||.|||
Db          8 AGTATGA 14


RESULT 10
AR082813
LOCUS       AR082813                  14 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 27 from patent US 5976789.
ACCESSION   AR082813
VERSION     AR082813.1  GI:10009603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
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```
  AUTHORS   Allibert,P.Andre., Cros,P., Mach,B.Francois., Mandrand,B.Fabien.
            and Tiercy,J.-M.
  TITLE     System of probes enabling HLA-DR typing to be performed, and typing
            method using said probes
  JOURNAL   Patent: US 5976789-A 27 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
BASE COUNT        6 a      1 c      4 g      3 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          8 AGTATGA 14


RESULT 11
AR088823/c
LOCUS       AR088823                 14 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5990294.
ACCESSION   AR088823
VERSION     AR088823.1  GI:10015586
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Murphy,G.P., Boynton,A.L. and Sehgal,A.
  TITLE     Nucleotide and amino acid sequences of C4-2, a tumor suppressor
            gene, and methods of use thereof
  JOURNAL   Patent: US 5990294-A 4 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
BASE COUNT        2 a      4 c      2 g      5 t      1 others
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         14 AGTATGA 8


RESULT 12
AX018748/c
LOCUS       AX018748                 14 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9943848.
ACCESSION   AX018748
VERSION     AX018748.1  GI:10042871
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Ong,C.J. and Jirik,F.R.
  TITLE     Protein interaction and transcription factor trap
  JOURNAL   Patent: WO 9943848-A 6 02-SEP-1999;
            ONG CHRISTOPHER J (CA); UNIV BRITISH COLUMBIA (CA); JIRIK FRANK R
            (CA)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligomer for adjusting a reading frame for
                     ligation"
BASE COUNT        3 a      4 c      2 g      5 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          7 AGTATGA 1


RESULT 13
AX343036/c
LOCUS       AX343036                 14 bp    DNA     linear   PAT 12-JAN-2002
DEFINITION  Sequence 22 from Patent WO0198350.
ACCESSION   AX343036
VERSION     AX343036.1  GI:18152236
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reinhard,C., Jefferson,A.B., Winter,J.A. and Randazzo,F.
  TITLE     Compositions and methods for treating neoplastic disease using net
            -4 modulators
  JOURNAL   Patent: WO 0198350-A 22 27-DEC-2001;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide NET-4 oligo 868 used for in-situ
                     hybridization"
BASE COUNT        3 a      4 c      2 g      5 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         13 AGTATGA 7


RESULT 14
A33153
LOCUS       A33153                   15 bp    DNA     linear   PAT 07-MAY-1996
DEFINITION  Synthetic HLA DR typing probe.
ACCESSION   A33153
VERSION     A33153.1  GI:1567737
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      1 c      5 g      3 t
ORIGIN

  Query Match            100.0%;  Score 7;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 15


RESULT 15
AR041154/c
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LOCUS       AR041154                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5811270.
ACCESSION   AR041154
VERSION     AR041154.1  GI:5961650
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grandgenett,D.P.
  TITLE     In vitro method for concerted integration of donor DNA molecules
            using retroviral integrase proteins
  JOURNAL   Patent: US 5811270-A 2 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        2 a      4 c      4 g      5 t
ORIGIN

  Query Match           100.0%;  Score 7;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 3


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GenCore version 5.1.6

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Title: US-09-540-843-1
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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37: em_htg_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		9	100.0	9	6	AX268753	AX268753 Sequence
2	c	9	100.0	15	6	AR130719	AR130719 Sequence
3	c	9	100.0	15	6	AR130720	AR130720 Sequence
4	c	9	100.0	17	6	AR039517	AR039517 Sequence
5	c	9	100.0	17	6	AR039519	AR039519 Sequence
6	c	9	100.0	17	6	AR039521	AR039521 Sequence
7	c	9	100.0	17	6	AR039523	AR039523 Sequence
8	c	9	100.0	18	6	AX306555	AX306555 Sequence
9		9	100.0	20	6	AR116520	AR116520 Sequence
10		9	100.0	20	6	AR116521	AR116521 Sequence
11	c	9	100.0	22	6	AX338664	AX338664 Sequence
12	c	9	100.0	23	6	AX404121	AX404121 Sequence
13		9	100.0	25	6	AX454970	AX454970 Sequence
14	c	9	100.0	25	6	E13462	E13462 PCR primer
15		9	100.0	26	6	AX112180	AX112180 Sequence
16		9	100.0	26	6	AX327686	AX327686 Sequence
17	c	9	100.0	27	6	AX115612	AX115612 Sequence
18		9	100.0	30	6	I08713	I08713 Sequence 1
19		9	100.0	31	6	A87084	A87084 Sequence 12
20		9	100.0	31	6	A87152	A87152 Sequence 12
21		9	100.0	31	6	AX229078	AX229078 Sequence
22		9	100.0	31	6	AX249534	AX249534 Sequence
23		9	100.0	32	6	AX339727	AX339727 Sequence
24	c	9	100.0	33	6	AX281025	AX281025 Sequence
25	c	9	100.0	33	6	AX281060	AX281060 Sequence
26	c	9	100.0	33	6	AX463705	AX463705 Sequence
27		9	100.0	34	6	AR080618	AR080618 Sequence
28	c	9	100.0	34	6	AX416939	AX416939 Sequence
29		9	100.0	36	6	A87098	A87098 Sequence 8
30		9	100.0	36	6	A87126	A87126 Sequence 36
31		9	100.0	36	6	AR206352	AR206352 Sequence
32		9	100.0	36	6	AR206380	AR206380 Sequence
33		9	100.0	36	6	AX300708	AX300708 Sequence
34		9	100.0	37	6	A87090	A87090 Sequence 18
35		9	100.0	37	6	A87160	A87160 Sequence 20
36		9	100.0	38	6	A87076	A87076 Sequence 4
37		9	100.0	38	6	A87120	A87120 Sequence 30
38		9	100.0	38	6	A87144	A87144 Sequence 4
39		9	100.0	38	6	A87171	A87171 Sequence 6
40		9	100.0	38	6	AR159979	AR159979 Sequence
41		9	100.0	38	6	AR206374	AR206374 Sequence
42		9	100.0	38	6	AX028965	AX028965 Sequence
43		9	100.0	39	6	A87099	A87099 Sequence 9
44		9	100.0	39	6	AR183718	AR183718 Sequence
45		9	100.0	39	6	AR206353	AR206353 Sequence

ALIGNMENTS

RESULT 1
AX268753
LOCUS AX268753 9 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0174342.
ACCESSION AX268753
VERSION AX268753.1 GI:16541825
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 1 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

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FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      4 g      2 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+09;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 2
AR130719/c
LOCUS       AR130719                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 6 from patent US 6190866.
ACCESSION   AR130719
VERSION     AR130719.1  GI:14119044
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nielsen,P.E. and Good,L.
  TITLE     Methods of bacterial gene function determination using peptide
            nucleic acids
  JOURNAL   Patent: US 6190866-A 6 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
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Db         11 GAGTATGAG 3


RESULT 3
AR130720/c
LOCUS       AR130720                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6190866.
ACCESSION   AR130720
VERSION     AR130720.1  GI:14119045
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nielsen,P.E. and Good,L.
  TITLE     Methods of bacterial gene function determination using peptide
            nucleic acids
  JOURNAL   Patent: US 6190866-A 7 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        5 a      4 c      1 g      5 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         14 GAGTATGAG 6


RESULT 4
AR039517/c
LOCUS       AR039517                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 365 from patent US 5807743.
ACCESSION   AR039517
VERSION     AR039517.1  GI:5958880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 365 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      7 c      2 g      5 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         17 GAGTATGAG 9


RESULT 5
AR039519/c
LOCUS       AR039519                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 367 from patent US 5807743.
ACCESSION   AR039519
VERSION     AR039519.1  GI:5958882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 367 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      7 c      2 g      5 t
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  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         15 GAGTATGAG 7


RESULT 6
AR039521/c
LOCUS       AR039521                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 369 from patent US 5807743.
ACCESSION   AR039521
VERSION     AR039521.1  GI:5958884
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
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  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 369 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT       3 a      8 c      1 g      5 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 17;
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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         12 GAGTATGAG 4


RESULT 7
AR039523/c
LOCUS       AR039523                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 371 from patent US 5807743.
ACCESSION   AR039523
VERSION     AR039523.1  GI:5958886
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 371 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT       4 a      9 c      0 g      4 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 1


RESULT 8
AX306555/c
LOCUS       AX306555                 18 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 1 from Patent WO0187285.
ACCESSION   AX306555
VERSION     AX306555.1  GI:17645773
KEYWORDS    .
SOURCE      black rat.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Johns,R.A. and Tao,Y.C.
  TITLE     Inhibition of the interaction of psd93 and psd95 with the nnos and
            nmda receptors
  JOURNAL   Patent: WO 0187285-A 1 22-NOV-2001;
            The Johns Hopkins University (US) ; Johns, Roger A. (US) ; Tao,
            Yuanxiang (US)
FEATURES             Location/Qualifiers
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BASE COUNT       3 a      6 c      2 g      7 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         18 GAGTATGAG 10


RESULT 9
AR116520
LOCUS       AR116520                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 101 from patent US 6133246.
ACCESSION   AR116520
VERSION     AR116520.1  GI:14096842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 101 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       4 a      3 c      7 g      6 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.3e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 10
AR116521
LOCUS       AR116521                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 102 from patent US 6133246.
ACCESSION   AR116521
VERSION     AR116521.1  GI:14096843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 102 17-OCT-2000;
FEATURES             Location/Qualifiers
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BASE COUNT       5 a      3 c      7 g      5 t
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Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 11
AX338664/c
LOCUS       AX338664                 22 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 29 from Patent WO0164713.
```

```
ACCESSION   AX338664
VERSION     AX338664.1  GI:18129026
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gasche,C., Zakeri,S.M. and Reinisch,W.
  TITLE     Mammalian interleukin-10 (il-10) receptor variants
  JOURNAL   Patent: WO 0164713-A 29 07-SEP-2001;
            Gasche, Christoph (AT) ; Zakeri, Schaker M. (AT)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        6 a      6 c      5 g      5 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.3e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         15 GAGTATGAG 7


RESULT 12
AX404121/c
LOCUS       AX404121                  23 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 17 from Patent WO0222819.
ACCESSION   AX404121
VERSION     AX404121.1  GI:21437421
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sonderegger,P., Hintsch,G., Kinter,J., Meskenaite,V., Schrimpf,S.,
            Vogt,L. and Zurlinden,A.
  TITLE     Calcium binding proteins
  JOURNAL   Patent: WO 0222819-A 17 21-MAR-2002;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .23
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                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        6 a      8 c      3 g      5 t      1 others
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.3e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         20 GAGTATGAG 12


RESULT 13
AX454970
LOCUS       AX454970                  25 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 37 from Patent WO0208453.
ACCESSION   AX454970
VERSION     AX454970.1  GI:21714155
KEYWORDS    .
SOURCE      dog.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1
  AUTHORS   Farr,S.B., Pickett,G.G., Neft,R.E. and Dunn,R.T.
  TITLE     Canine toxicity genes
  JOURNAL   Patent: WO 0208453-A 37 31-JAN-2002;
            Phase-1 Molecular Toxicology (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
BASE COUNT        8 a      2 c     10 g      5 t
ORIGIN

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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 14
E13462/c
LOCUS       E13462                    25 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  PCR primer for detecting mRNA which encode human cholecystokinin/
            pancreozymin.
ACCESSION   E13462
VERSION     E13462.1  GI:3252267
KEYWORDS    JP 1997187299-A/24.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kimoto,Y.
  TITLE     PRIMER FOR PCR
  JOURNAL   Patent: JP 1997187299-A 24 22-JUL-1997;
            NIPPON BIO SERAPII KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997187299-A/24
            PD   22-JUL-1997
            PF   05-JAN-1996 JP 1996027222
            PI   KIMOTO YASUHIKO
            PC   C12Q1/68,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .25
            FT                   /organism='Artificial sezuences' FT
            misc_feature    1. .25
            FT                   /note='PCR primer,CCK-4'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      8 c      6 g      6 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.2e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         24 GAGTATGAG 16


RESULT 15
AX112180
LOCUS       AX112180                  26 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 32 from Patent WO0127287.
```

```
ACCESSION   AX112180
VERSION     AX112180.1  GI:13939031
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Long,D.M., Metz,A.M. and Love,R.
  TITLE     Telomerase reverse transcriptase (tert) genes
  JOURNAL   Patent: WO 0127287-A 32 19-APR-2001;
            Research & Development Institute Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="RT-PCR primer used with P. falciparum sequences"
BASE COUNT        9 a      3 c      7 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.2e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         16 GAGTATGAG 24


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GenCore version 5.1.6

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Title: US-09-540-843-1
Perfect score: 9
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY_NUC
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	9	100.0	9	20	AAZ10692	Oligonucleotide se
	2	9	100.0	9	23	AAS14905	Melanogenesis asso
	3	9	100.0	12	23	ABI05192	Oligonucleotide pr
	4	9	100.0	12	23	ABI06838	Oligonucleotide pr
	5	9	100.0	12	23	ABI06839	Oligonucleotide pr
	6	9	100.0	12	23	ABI21133	Oligonucleotide pr
	7	9	100.0	12	23	ABI26099	Oligonucleotide pr
c	8	9	100.0	12	23	ABI48017	Oligonucleotide pr
	9	9	100.0	13	23	ABC29988	Oligonucleotide SE
c	10	9	100.0	13	23	ABC29989	Oligonucleotide SE
	11	9	100.0	13	23	ABC37140	Oligonucleotide SE
c	12	9	100.0	13	23	ABC37141	Oligonucleotide SE
	13	9	100.0	13	23	ABC41298	Oligonucleotide SE
c	14	9	100.0	13	23	ABC41299	Oligonucleotide SE
	15	9	100.0	13	23	ABC48092	Oligonucleotide SE
c	16	9	100.0	13	23	ABC48093	Oligonucleotide SE
	17	9	100.0	13	23	ABC51860	Oligonucleotide SE
c	18	9	100.0	13	23	ABC51861	Oligonucleotide SE
	19	9	100.0	13	23	ABC51864	Oligonucleotide SE
c	20	9	100.0	13	23	ABC51865	Oligonucleotide SE
	21	9	100.0	13	23	ABC78830	Oligonucleotide SE
c	22	9	100.0	13	23	ABC78831	Oligonucleotide SE
	23	9	100.0	13	23	ABC99290	Oligonucleotide SE
c	24	9	100.0	13	23	ABC99291	Oligonucleotide SE
	25	9	100.0	13	23	ABF09008	Oligonucleotide SE
c	26	9	100.0	13	23	ABF09009	Oligonucleotide SE
	27	9	100.0	13	23	ABF15710	Oligonucleotide SE
c	28	9	100.0	13	23	ABF15711	Oligonucleotide SE
	29	9	100.0	13	23	ABF17600	Oligonucleotide SE
c	30	9	100.0	13	23	ABF17601	Oligonucleotide SE
	31	9	100.0	13	23	ABF20572	Oligonucleotide SE
c	32	9	100.0	13	23	ABF20573	Oligonucleotide SE
	33	9	100.0	13	23	ABF20576	Oligonucleotide SE
c	34	9	100.0	13	23	ABF20577	Oligonucleotide SE
	35	9	100.0	13	23	ABF48816	Oligonucleotide SE
c	36	9	100.0	13	23	ABF48817	Oligonucleotide SE
	37	9	100.0	13	23	ABF56046	Oligonucleotide SE
c	38	9	100.0	13	23	ABF56047	Oligonucleotide SE
	39	9	100.0	13	23	ABF64312	Oligonucleotide SE
c	40	9	100.0	13	23	ABF64313	Oligonucleotide SE
	41	9	100.0	13	23	ABF64318	Oligonucleotide SE
c	42	9	100.0	13	23	ABF64319	Oligonucleotide SE
	43	9	100.0	13	23	ABF95900	Oligonucleotide SE
c	44	9	100.0	13	23	ABF95901	Oligonucleotide SE
	45	9	100.0	13	23	ABH11442	Oligonucleotide SE

ALIGNMENTS

RESULT 1
AAZ10692
ID AAZ10692 standard; DNA; 9 BP.
XX
AC AAZ10692;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 29; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 1 GAGTATGAG 9

RESULT 2
AAS14905
ID AAS14905 standard; DNA; 9 BP.
XX
AC AAS14905;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #1.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /note= "Optionally phosphorylated"
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #1, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 1 GAGTATGAG 9

RESULT 3
ABI05192
ID ABI05192 standard; DNA; 12 BP.
XX
AC ABI05192;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 305165 for detecting SNP TSC0021329.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 305165; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

```
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 4
ABI06838
ID   ABI06838 standard; DNA; 12 BP.
XX
AC   ABI06838;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 306811 for detecting SNP TSC0022179.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 306811; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          3 GAGTATGAG 11


RESULT 5
ABI06839
ID   ABI06839 standard; DNA; 12 BP.
XX
AC   ABI06839;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 306812 for detecting SNP TSC0022179.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 306812; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          3 GAGTATGAG 11


RESULT 6
ABI21133
ID   ABI21133 standard; DNA; 12 BP.
XX
AC   ABI21133;
XX
DT   22-FEB-2002  (first entry)
```

```
XX
DE   Oligonucleotide primer SEQ ID NO 321106 for detecting SNP TSC0030074.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 321106; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          2 GAGTATGAG 10


RESULT 7
ABI26099
ID   ABI26099 standard; DNA; 12 BP.
XX
AC   ABI26099;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 326072 for detecting SNP TSC0032886.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 326072; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          4 GAGTATGAG 12


RESULT 8
ABI48017/c
ID   ABI48017 standard; DNA; 12 BP.
XX
AC   ABI48017;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 347990 for detecting SNP TSC0045390.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
```

```
XX
PS   Claim 1; SEQ ID 347990; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         10 GAGTATGAG 2


RESULT 9
ABC29988
ID   ABC29988 standard; DNA; 13 BP.
XX
AC   ABC29988;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 30005 for detecting SNP TSC0009039.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 30005; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          4 GAGTATGAG 12


RESULT 10
ABC29989/c
ID   ABC29989 standard; DNA; 13 BP.
XX
AC   ABC29989;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 30006 for detecting SNP TSC0009039.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 30006; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         10 GAGTATGAG 2
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RESULT 11
ABC37140
ID   ABC37140 standard; DNA; 13 BP.
XX
AC   ABC37140;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37157 for detecting SNP TSC0011603.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 37157; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          3 GAGTATGAG 11


RESULT 12
ABC37141/c
ID   ABC37141 standard; DNA; 13 BP.
XX
AC   ABC37141;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37158 for detecting SNP TSC0011603.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 37158; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         11 GAGTATGAG 3


RESULT 13
ABC41298
ID   ABC41298 standard; DNA; 13 BP.
XX
AC   ABC41298;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 41315 for detecting SNP TSC0012414.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
```

XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 41315; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 5 GAGTATGAG 13

RESULT 14
ABC41299/c
ID ABC41299 standard; DNA; 13 BP.
XX
AC ABC41299;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 41316 for detecting SNP TSC0012414.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 41316; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 9 GAGTATGAG 1

RESULT 15
ABC48092
ID ABC48092 standard; DNA; 13 BP.
XX
AC ABC48092;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 48109 for detecting SNP TSC0013750.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 48109; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGTATGAG 9
              |||||||||
Db          5 GAGTATGAG 13
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Search completed: June 2, 2003, 18:45:09
Job time : 151.566 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:29:55 ; Search time 1129.39 Seconds
(without alignments)
129.060 Million cell updates/sec

Title: US-09-540-843-1
Perfect score: 9
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		9	100.0	22	17	AZ658158	AZ658158 1M0534H17
c 2		9	100.0	29	17	BH856420	BH856420 SALK_0797
3		9	100.0	36	17	AL771699	AL771699 Arabidops
c 4		9	100.0	40	9	AI613042	AI613042 ty06h09.x
c 5		8	88.9	24	10	AW059679	AW059679 AHuTH.bss
c 6		8	88.9	24	17	AZ478673	AZ478673 1M0298J20
c 7		8	88.9	25	17	AZ605844	AZ605844 1M0427J22
c 8		8	88.9	27	14	D45824	D45824 HUMGS03044
9		8	88.9	30	17	AL766985	AL766985 Arabidops
c 10		8	88.9	33	17	AZ778279	AZ778279 2M0013N15
11		8	88.9	33	17	TA307A09Q	AL488827 T. brucei
c 12		8	88.9	34	17	AZ333219	AZ333219 1M0062O09
13		8	88.9	36	17	AZ776722	AZ776722 2M0010A12
c 14		8	88.9	36	17	BH789482	BH789482 SALK_0297
c 15		8	88.9	37	9	AA088913	AA088913 z169b11.s
16		8	88.9	37	17	AZ429862	AZ429862 1M0214I05
17		8	88.9	37	17	BH847696	BH847696 SALK_0558
c 18		8	88.9	38	17	BH130009	BH130009 G-6f16.f
19		8	88.9	38	17	TA131D03P	AL464176 T. brucei
c 20		8	88.9	39	17	AZ659283	AZ659283 1M0536M03
21		8	88.9	39	17	BH846916	BH846916 SALK_0110
c 22		8	88.9	40	17	AZ311244	AZ311244 1M0026N06
c 23		7.4	82.2	17	13	BG926068	BG926068 HNC23-1-E
24		7.4	82.2	19	9	AI747751	AI747751 ul21h05.x
c 25		7.4	82.2	19	17	AZ358656	AZ358656 1M0101K12
c 26		7.4	82.2	19	17	AZ457990	AZ457990 1M0261E11
c 27		7.4	82.2	19	17	AZ991531	AZ991531 2M0275K15
28		7.4	82.2	20	17	AZ646291	AZ646291 1M0512D07
29		7.4	82.2	21	17	AZ806440	AZ806440 2M0068B05
c 30		7.4	82.2	22	9	AI052232	AI052232 oz21a12.x
c 31		7.4	82.2	22	9	AI630912	AI630912 tz31g03.x
32		7.4	82.2	22	17	AZ591103	AZ591103 1M0401K07
33		7.4	82.2	22	17	BH811671	BH811671 SALK_0595
c 34		7.4	82.2	22	17	TA119E04Q	AL463250 T. brucei
35		7.4	82.2	23	17	AZ484572	AZ484572 1M0311D10
36		7.4	82.2	23	17	AZ660131	AZ660131 1M0538H03
c 37		7.4	82.2	23	17	AZ830077	AZ830077 2M0109O06
c 38		7.4	82.2	24	17	AZ370614	AZ370614 1M0121O10
c 39		7.4	82.2	24	17	AZ772496	AZ772496 1M0583I23
40		7.4	82.2	24	17	AZ847502	AZ847502 2M0148C08
c 41		7.4	82.2	24	17	BH865517	BH865517 SALK_0987
42		7.4	82.2	25	9	AA871952	AA871952 vq43b09.r
43		7.4	82.2	25	17	AZ810630	AZ810630 2M0076I14
44		7.4	82.2	25	17	AZ831709	AZ831709 2M0111O06
c 45		7.4	82.2	25	17	BH856297	BH856297 SALK_0810

ALIGNMENTS

RESULT 1
AZ658158
LOCUS AZ658158 22 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0534H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0534H17 R, DNA sequence.
ACCESSION AZ658158
VERSION AZ658158.1 GI:11795304
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: H column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0534H17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 0 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 9; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 12 GAGTATGAG 20

RESULT 2
BH856420/c
LOCUS BH856420 29 bp DNA linear GSS 08-JUL-2002
DEFINITION SALK_079762.18.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_079762.18.10.x, DNA sequence.
ACCESSION BH856420
VERSION BH856420.1 GI:21706010
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P. , Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g63570.
Class: TDNA tagged.

FEATURES Location/Qualifiers
source 1. .29
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_079762.18.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 6 a 10 c 4 g 9 t
ORIGIN

Query Match 100.0%; Score 9; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 22 GAGTATGAG 14

RESULT 3
AL771699
LOCUS AL771699 36 bp DNA linear GSS 19-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-182E01-013594, genomic survey sequence.
ACCESSION AL771699
VERSION AL771699.1 GI:21533901
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 36)
AUTHORS Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f15n24. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES Location/Qualifiers
source 1. .36
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-182E01-013594"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 9 a 8 c 6 g 13 t
ORIGIN

Query Match 100.0%; Score 9; DB 17; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 2 GAGTATGAG 10

RESULT 4
AI613042/c
LOCUS AI613042 40 bp mRNA linear EST 16-DEC-1999
DEFINITION ty06h09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2278337 3' similar to SW:RL11_PIG Q29205 60S RIBOSOMAL PROTEIN L11 ;, mRNA sequence.
ACCESSION AI613042
VERSION AI613042.1 GI:4622209
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 705 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES Location/Qualifiers
source 1. .40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2278337"
/clone_lib="NCI_CGAP_Ut3"
/tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"
BASE COUNT 9 a 15 c 3 g 13 t
ORIGIN

Query Match 100.0%; Score 9; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 16 GAGTATGAG 8

RESULT 5
AW059679/c
LOCUS AW059679 24 bp mRNA linear EST 23-AUG-2000
DEFINITION AHuTH.bsst.dnc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW059679
VERSION AW059679.1 GI:6652001
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
MEDLINE 20144098
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate.
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DNC15"
/cell_type="monocyctic leukemia"
/cell_line="THP-1 (TIB-202)"
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only). "
BASE COUNT 9 a 6 c 1 g 8 t
ORIGIN

Query Match 88.9%; Score 8; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGA 8
||||||||
Db 24 GAGTATGA 17

RESULT 6
AZ478673/c
LOCUS AZ478673 24 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0298J20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0298J20 R, DNA sequence.
ACCESSION AZ478673
VERSION AZ478673.1 GI:10637794
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0298  row: J  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0298J20"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        6 a      8 c      3 g      7 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGTATGAG 9
              ||||||||
Db          8 AGTATGAG 1


RESULT 7
AZ605844/c
LOCUS       AZ605844                 25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0427J22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0427J22 F, DNA sequence.
ACCESSION   AZ605844
VERSION     AZ605844.1  GI:11728034
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0427  row: J  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0427J22"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        7 a      6 c      5 g      7 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGTATGAG 9
              ||||||||
Db         17 AGTATGAG 10


RESULT 8
D45824/c
LOCUS       D45824                   27 bp    mRNA    linear   EST 21-FEB-1995
DEFINITION  HUMGS03044 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA
            3', mRNA sequence.
ACCESSION   D45824
VERSION     D45824.1  GI:662778
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.
  TITLE     An expression profile of active genes in human lung
  JOURNAL   DNA Res. 1, 279-287 (1994)
  MEDLINE   95236275
COMMENT     Contact: Kohichi Itoh
            Institute for Molecular and Cellular Biology
            Osaka University
```

```
            3-1, Yamadaoka, Suita, Osaka, 565, Japan
            Tel: 06-877-5111 x3910
            Fax: 06-877-1922.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult lung 3' directed MboI cDNA"
                     /note="Adult human lung, 3' directed MboI"
BASE COUNT       12 a      6 c      1 g      8 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 14;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGA 8
              ||||||||
Db         24 GAGTATGA 17


RESULT 9
AL766985
LOCUS       AL766985                 30 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-215C11-014144,
            genomic survey sequence.
ACCESSION   AL766985
VERSION     AL766985.1  GI:21520104
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 30)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F9L1. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-215C11-014144"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT       11 a      5 c      4 g      10 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGA 8
              ||||||||
Db         19 GAGTATGA 26


RESULT 10
AZ778279/c
LOCUS       AZ778279                 33 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0013N15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0013N15 F, DNA sequence.
ACCESSION   AZ778279
VERSION     AZ778279.1  GI:12907753
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0013  row: N  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0013N15"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
```

and selected for ampicillin resistance."
BASE COUNT 14 a 9 c 3 g 7 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGTATGAG 9
||||||||
Db 23 AGTATGAG 16

RESULT 11
TA307A09Q
LOCUS TA307A09Q 33 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 307a09, reverse sequence, genomic survey sequence.
ACCESSION AL488827
VERSION AL488827.1 GI:11864397
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .33
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="307a09"
BASE COUNT 7 a 6 c 10 g 10 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGA 8
||||||||
Db 8 GAGTATGA 15

RESULT 12
AZ333219/c
LOCUS AZ333219 34 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062O09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0062O09 F, DNA sequence.
ACCESSION AZ333219
VERSION AZ333219.1 GI:10397621
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 34)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: O column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
FEATURES Location/Qualifiers
source 1. .34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0062O09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 13 a 6 c 4 g 11 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGTATGAG 9
||||||||
Db 22 AGTATGAG 15

RESULT 13
AZ776722
LOCUS AZ776722 36 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0010A12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0010A12 R, DNA sequence.
ACCESSION AZ776722
VERSION AZ776722.1 GI:12904580
KEYWORDS GSS.
SOURCE house mouse.

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0010  row: A  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0010A12"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a      4 c      8 g     11 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGTATGAG 9
              ||||||||
Db         10 AGTATGAG 17


RESULT 14
BH789482/c
LOCUS       BH789482                 36 bp    DNA     linear   GSS 02-APR-2002
DEFINITION  SALK_029703.49.45.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_029703.49.45.x, DNA
            sequence.
ACCESSION   BH789482
VERSION     BH789482.1  GI:19882580
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_029703.49.45.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       10 a      6 c      7 g     13 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGA 8
              ||||||||
Db         28 GAGTATGA 21


RESULT 15
AA088913/c
LOCUS       AA088913                 37 bp    mRNA    linear   EST 19-MAY-1997
DEFINITION  z169b11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
            IMAGE:509853 3' similar to TR:G189397 G189397 HYPOTHETICAL 33.4 KD
            PROTEIN. ;, mRNA sequence.
ACCESSION   AA088913
VERSION     AA088913.1  GI:1633677
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

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           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Insert Length: 1260   Std Error: 0.00
           Seq primer: -40M13 fwd. from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="GDB:3813185"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:509853"
                     /clone_lib="Stratagene colon (#937204)"
                     /tissue_type="tumor"
                     /cell_line="T84 carcinoma cell line"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: colon; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. T-84 colonic epithelial cell line.  Average
                     insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT        7 a     10 c     10 g      9 t      1 others
ORIGIN

  Query Match             88.9%;  Score 8;  DB 9;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGA 8
              ||||||||
Db         22 GAGTATGA 15


Search completed: June  2, 2003, 20:35:33
Job time : 1133.39 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:31:20 ; Search time 36.878 Seconds
(without alignments)
74.844 Million cell updates/sec

Title: US-09-540-843-1
Perfect score: 9
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	3	US-09-048-927-1	Sequence 1, Appli
c	2	9	100.0	15	4	US-09-049-190-6	Sequence 6, Appli
c	3	9	100.0	15	4	US-09-049-190-7	Sequence 7, Appli
c	4	9	100.0	15	4	US-08-932-140C-6	Sequence 6, Appli
c	5	9	100.0	15	4	US-08-932-140C-7	Sequence 7, Appli
c	6	9	100.0	17	1	US-08-758-306-365	Sequence 365, App
c	7	9	100.0	17	1	US-08-758-306-367	Sequence 367, App
c	8	9	100.0	17	1	US-08-758-306-369	Sequence 369, App
c	9	9	100.0	17	1	US-08-758-306-371	Sequence 371, App
	10	9	100.0	20	3	US-09-287-796-101	Sequence 101, App
	11	9	100.0	20	3	US-09-287-796-102	Sequence 102, App
	12	9	100.0	20	4	US-09-130-616-101	Sequence 101, App
	13	9	100.0	20	4	US-09-130-616-102	Sequence 102, App
	14	9	100.0	20	4	US-09-105-058C-15	Sequence 15, Appl
c	15	9	100.0	20	4	US-09-851-062-29	Sequence 29, Appl
c	16	9	100.0	20	4	US-09-517-467B-84	Sequence 84, Appl
	17	9	100.0	21	6	5455029-26	Patent No. 5455029
c	18	9	100.0	23	4	US-09-088-274-8	Sequence 8, Appli
	19	9	100.0	24	4	US-09-245-248B-23	Sequence 23, Appl
	20	9	100.0	27	4	US-08-932-140C-21	Sequence 21, Appl
c	21	9	100.0	28	4	US-09-031-006-4	Sequence 4, Appli
	22	9	100.0	34	2	US-08-211-718-14	Sequence 14, Appl
	23	9	100.0	36	4	US-09-383-143-8	Sequence 8, Appli
	24	9	100.0	36	4	US-09-383-143-36	Sequence 36, Appl
	25	9	100.0	37	1	US-08-029-030-1	Sequence 1, Appli
	26	9	100.0	37	6	5455029-3	Patent No. 5455029
	27	9	100.0	38	4	US-09-194-613-18	Sequence 18, Appl
	28	9	100.0	38	4	US-09-383-143-30	Sequence 30, Appl
	29	9	100.0	39	3	US-08-980-032-4	Sequence 4, Appli
	30	9	100.0	39	4	US-09-477-871-4	Sequence 4, Appli
	31	9	100.0	39	4	US-09-383-143-9	Sequence 9, Appli
c	32	9	100.0	40	2	US-08-425-684-27	Sequence 27, Appl
	33	9	100.0	40	2	US-08-425-684-34	Sequence 34, Appl
c	34	9	100.0	40	2	US-08-675-502-27	Sequence 27, Appl
	35	9	100.0	40	2	US-08-675-502-34	Sequence 34, Appl
c	36	8	88.9	14	2	US-08-744-905A-4	Sequence 4, Appli
	37	8	88.9	15	1	US-08-334-847-24	Sequence 24, Appl
c	38	8	88.9	15	2	US-08-747-121-4	Sequence 4, Appli
	39	8	88.9	15	2	US-08-585-684B-1315	Sequence 1315, Ap
	40	8	88.9	15	4	US-09-038-073-1315	Sequence 1315, Ap
c	41	8	88.9	16	1	US-07-977-284A-59	Sequence 59, Appl
c	42	8	88.9	16	2	US-08-256-426B-59	Sequence 59, Appl
	43	8	88.9	17	3	US-08-985-162-443	Sequence 443, App
	44	8	88.9	17	3	US-08-985-162-444	Sequence 444, App
	45	8	88.9	18	1	US-07-688-352C-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-048-927-1
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-1

  Query Match             100.0%;  Score 9;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 2
US-09-049-190-6/c
; Sequence 6, Application US/09049190
; Patent No. 6190866
;  GENERAL INFORMATION:
;    APPLICANT:  Nielsen et al.
;    TITLE OF INVENTION:  Peptide Nucleic Acids Having
;    TITLE OF INVENTION:  Antibacterial Activity
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz          & No. 6190866ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
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; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
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; LOCATION: 8
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
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; NAME/KEY: Modified-site
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; OTHER INFORMATION: backbone
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; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
; OTHER INFORMATION: backbone
US-09-049-190-6

Query Match 100.0%; Score 9; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
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Db 11 GAGTATGAG 3

RESULT 3
US-09-049-190-7/c
; Sequence 7, Application US/09049190
; Patent No. 6190866
; GENERAL INFORMATION:
; APPLICANT: Nielsen et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having
; TITLE OF INVENTION: Antibacterial Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6190866ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100

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;       TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
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;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
;      OTHER INFORMATION:  N-[acetyl(2-aminoethyl)]-C-lysine-glycine
;      OTHER INFORMATION:  backbone
US-09-049-190-7

  Query Match             100.0%;  Score 9;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         14 GAGTATGAG 6


RESULT 4
US-08-932-140C-6/c
; Sequence 6, Application US/08932140C
; Patent No. 6300318
;  GENERAL INFORMATION:
;    APPLICANT:  Nielsen et al.
;    TITLE OF INVENTION:  Peptide Nucleic Acids Having
;    TITLE OF INVENTION:  Antibacterial Activity
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  No. 6300318ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/932,140C
;      FILING DATE:  Septemeber 16, 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John W. Caldwell
;      REGISTRATION NUMBER:  28,937
;      REFERENCE/DOCKET NUMBER:  ISIS-2560
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
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;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  5
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  6
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  7
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  8
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  9
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
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;       NAME/KEY:  Modified-site
;       LOCATION:  10
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
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;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  12
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  13
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  14
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  N-[acetyl(2-aminoethyl)]-C-
;       OTHER INFORMATION:  lysine-glycine backbone
US-08-932-140C-6

  Query Match             100.0%;  Score 9;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         11 GAGTATGAG 3


RESULT 5
US-08-932-140C-7/c
; Sequence 7, Application US/08932140C
; Patent No. 6300318
;  GENERAL INFORMATION:
;    APPLICANT:  Nielsen et al.
;    TITLE OF INVENTION:  Peptide Nucleic Acids Having
;    TITLE OF INVENTION:  Antibacterial Activity
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  No. 6300318ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/932,140C
;      FILING DATE:  Septemeber 16, 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John W. Caldwell
;      REGISTRATION NUMBER:  28,937
;      REFERENCE/DOCKET NUMBER:  ISIS-2560
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
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;       LOCATION:  9
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
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;       LOCATION:  10
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
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;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  12
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  13
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  14
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  N-[acetyl(2-aminoethyl)]-C-
;       OTHER INFORMATION:  lysine-glycine backbone
US-08-932-140C-7

  Query Match             100.0%;  Score 9;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         14 GAGTATGAG 6


RESULT 6
US-08-758-306-365/c
; Sequence 365, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  365:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-365

  Query Match             100.0%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         17 GAGTATGAG 9


RESULT 7
US-08-758-306-367/c
; Sequence 367, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  367:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-367

  Query Match            100.0%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         15 GAGTATGAG 7


RESULT 8
US-08-758-306-369/c
; Sequence 369, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  369:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-369

  Query Match            100.0%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         12 GAGTATGAG 4


RESULT 9
US-08-758-306-371/c
; Sequence 371, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  371:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-371

  Query Match            100.0%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 1


RESULT 10
US-09-287-796-101
; Sequence 101, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
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; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 101
;  LENGTH: 20
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic Sequence
US-09-287-796-101

  Query Match             100.0%;  Score 9;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 11
US-09-287-796-102
; Sequence 102, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0350
;  CURRENT APPLICATION NUMBER: US/09/287,796A
;  CURRENT FILING DATE: 1999-04-07
;  EARLIER APPLICATION NUMBER: 09/130,616
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 102
;  LENGTH: 20
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic Sequence
US-09-287-796-102

  Query Match             100.0%;  Score 9;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 12
US-09-130-616-101
; Sequence 101, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 101
;  LENGTH: 20
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic sequence
US-09-130-616-101

  Query Match             100.0%;  Score 9;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 13
US-09-130-616-102
; Sequence 102, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett
;  APPLICANT: Nero, Pam
;  APPLICANT: Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0318
;  CURRENT APPLICATION NUMBER: US/09/130,616C
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 08/910,629
;  EARLIER FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 102
;  LENGTH: 20
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Synthetic sequence
US-09-130-616-102

  Query Match             100.0%;  Score 9;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 14
US-09-105-058C-15
; Sequence 15, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
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;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Forward primer
;   OTHER INFORMATION: from EST sequence similar to the KvLQT gene
US-09-105-058C-15

  Query Match           100.0%;  Score 9;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 15
US-09-851-062-29/c
; Sequence 29, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-29

  Query Match           100.0%;  Score 9;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         19 GAGTATGAG 11


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Job time : 37.878 secs
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GenCore version 5.1.6

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(without alignments)
189.976 Million cell updates/sec

Title: US-09-540-843-1
Perfect score: 9
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 477662

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Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	9	US-10-122-630-1	Sequence 1, Appli
	2	9	100.0	9	9	US-10-122-633-1	Sequence 1, Appli
	3	9	100.0	17	10	US-09-866-108-2750	Sequence 2750, Ap
	4	9	100.0	17	10	US-09-866-108-2751	Sequence 2751, Ap
	5	9	100.0	17	10	US-09-866-108-2752	Sequence 2752, Ap
	6	9	100.0	17	10	US-09-866-108-2753	Sequence 2753, Ap
	7	9	100.0	17	10	US-09-866-108-2754	Sequence 2754, Ap
	8	9	100.0	17	10	US-09-866-108-2755	Sequence 2755, Ap
	9	9	100.0	17	10	US-09-866-108-2756	Sequence 2756, Ap
	10	9	100.0	17	10	US-09-866-108-2757	Sequence 2757, Ap
	11	9	100.0	17	10	US-09-866-108-2758	Sequence 2758, Ap
c	12	9	100.0	18	10	US-09-853-895-1	Sequence 1, Appli
	13	9	100.0	20	9	US-10-128-870-15	Sequence 15, Appl
	14	9	100.0	20	9	US-09-774-809-101	Sequence 101, App
	15	9	100.0	20	9	US-09-774-809-102	Sequence 102, App
	16	9	100.0	20	9	US-10-131-685-15	Sequence 15, Appl
c	17	9	100.0	20	9	US-10-067-514-32	Sequence 32, Appl
	18	9	100.0	24	10	US-09-815-656-23	Sequence 23, Appl
	19	9	100.0	25	9	US-10-215-112-4205	Sequence 4205, Ap
	20	9	100.0	25	9	US-10-215-112-4329	Sequence 4329, Ap
c	21	9	100.0	25	9	US-10-215-112-10765	Sequence 10765, A
c	22	9	100.0	25	9	US-10-215-112-10891	Sequence 10891, A
	23	9	100.0	25	9	US-09-911-904-37	Sequence 37, Appl
	24	9	100.0	25	10	US-09-866-108-5679	Sequence 5679, Ap
	25	9	100.0	25	10	US-09-866-108-5680	Sequence 5680, Ap
	26	9	100.0	25	10	US-09-866-108-5681	Sequence 5681, Ap
	27	9	100.0	25	10	US-09-866-108-5682	Sequence 5682, Ap
	28	9	100.0	25	10	US-09-866-108-5683	Sequence 5683, Ap
	29	9	100.0	25	10	US-09-866-108-5684	Sequence 5684, Ap
	30	9	100.0	25	10	US-09-866-108-5685	Sequence 5685, Ap
	31	9	100.0	25	10	US-09-866-108-5686	Sequence 5686, Ap
	32	9	100.0	25	10	US-09-866-108-5687	Sequence 5687, Ap
	33	9	100.0	25	10	US-09-866-108-5688	Sequence 5688, Ap
	34	9	100.0	25	10	US-09-866-108-5689	Sequence 5689, Ap
	35	9	100.0	25	10	US-09-866-108-5690	Sequence 5690, Ap
	36	9	100.0	25	10	US-09-866-108-5691	Sequence 5691, Ap
	37	9	100.0	25	10	US-09-866-108-5692	Sequence 5692, Ap
	38	9	100.0	25	10	US-09-866-108-5693	Sequence 5693, Ap
	39	9	100.0	25	10	US-09-866-108-5694	Sequence 5694, Ap
	40	9	100.0	25	10	US-09-866-108-5695	Sequence 5695, Ap
	41	9	100.0	31	9	US-09-776-474-2450	Sequence 2450, Ap
	42	9	100.0	31	10	US-09-801-274-1613	Sequence 1613, Ap
	43	9	100.0	32	9	US-10-014-101-24	Sequence 24, Appl
c	44	9	100.0	33	10	US-09-828-313-59	Sequence 59, Appl
c	45	9	100.0	33	10	US-09-828-313-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-10-122-630-1
; Sequence 1, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

Query Match 100.0%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 1 GAGTATGAG 9

```
RESULT 2
US-10-122-633-1
; Sequence 1, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

  Query Match             100.0%;  Score 9;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+08;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 3
US-09-866-108-2750
; Sequence 2750, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2750
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2750

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 4
US-09-866-108-2751
; Sequence 2751, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
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;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2751
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2751

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          8 GAGTATGAG 16


RESULT 5
US-09-866-108-2752
; Sequence 2752, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2752
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2752

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          7 GAGTATGAG 15


RESULT 6
US-09-866-108-2753
; Sequence 2753, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2753
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2753

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          6 GAGTATGAG 14


RESULT 7
US-09-866-108-2754
; Sequence 2754, Application US/09866108
; Patent No. US20020048800A1
```

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; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2754
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2754

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          5 GAGTATGAG 13


RESULT 8
US-09-866-108-2755
; Sequence 2755, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2755
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2755

  Query Match             100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          4 GAGTATGAG 12


RESULT 9
US-09-866-108-2756
; Sequence 2756, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2756
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2756

Query Match 100.0%; Score 9; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGTATGAG 9
              |||||||||
Db          3 GAGTATGAG 11
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RESULT 10
US-09-866-108-2757
; Sequence 2757, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2757
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2757

Query Match 100.0%; Score 9; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGTATGAG 9
              |||||||||
Db          2 GAGTATGAG 10
```

RESULT 11
US-09-866-108-2758
; Sequence 2758, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

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;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2758
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2758

  Query Match           100.0%;  Score 9;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 12
US-09-853-895-1/c
; Sequence 1, Application US/09853895
; Patent No. US20020045590A1
; GENERAL INFORMATION:
;  APPLICANT: Johns, Roger
;  APPLICANT:  Tao, Yuan-Xiang
;  TITLE OF INVENTION: Inhibition of interaction of PSD93 and
;  TITLE OF INVENTION:  PSD95 with nNOS and NMDA receptors
;  FILE REFERENCE: 01107.00130
;  CURRENT APPLICATION NUMBER: US/09/853,895
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: 60/242590
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/203894
;  PRIOR FILING DATE: 2000-05-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Rattus rattus
US-09-853-895-1

  Query Match           100.0%;  Score 9;  DB 10;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db         18 GAGTATGAG 10


RESULT 13
US-10-128-870-15
; Sequence 15, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
;  APPLICANT: Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE: DC58aDIV
;  CURRENT APPLICATION NUMBER: US/10/128,870
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 09/105,058
;  PRIOR FILING DATE: June 26, 1998
;  PRIOR APPLICATION NUMBER: 60/055,599
;  PRIOR FILING DATE: August 12, 1997
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Forward
;   OTHER INFORMATION: primer from EST sequence similar to the KvLQT gene
US-10-128-870-15

  Query Match           100.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          1 GAGTATGAG 9


RESULT 14
US-09-774-809-101
; Sequence 101, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett
;  APPLICANT:  Nero, Pam
;  APPLICANT:  Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION:  FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0412
;  CURRENT APPLICATION NUMBER: US/09/774,809
;  CURRENT FILING DATE:  2001-01-31
;  PRIOR APPLICATION NUMBER: 09/396,902
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 09/130,616
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 08/910,629
;  PRIOR FILING DATE: 1997-08-03
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 101
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-774-809-101

  Query Match           100.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGTATGAG 9
              |||||||||
Db          9 GAGTATGAG 17


RESULT 15
US-09-774-809-102
; Sequence 102, Application US/09774809
; Publication No. US20030004120A1
; GENERAL INFORMATION:
;  APPLICANT: McKay, Robert A.
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett
;  APPLICANT:  Nero, Pam
;  APPLICANT:  Gaarde, William A.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
;  TITLE OF INVENTION:  FOR THE MODULATION OF JNK PROTEINS
;  FILE REFERENCE: ISPH-0412
;  CURRENT APPLICATION NUMBER: US/09/774,809
;  CURRENT FILING DATE:  2001-01-31
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; PRIOR APPLICATION NUMBER: 09/396,902
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/130,616
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 08/910,629
; PRIOR FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-774-809-102

Query Match 100.0%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
|||||||||
Db 9 GAGTATGAG 17

Search completed: June 2, 2003, 23:43:11
Job time : 64.8781 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 17:32:40 ; Search time 150.366 Seconds
(without alignments)
134.791 Million cell updates/sec

Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	20	AAZ10693	Oligonucleotide se
	2	9	100.0	9	23	AAS14906	Melanogenesis asso
	3	9	100.0	12	23	ABH73149	Oligonucleotide pr
c	4	9	100.0	12	23	ABH79033	Oligonucleotide pr
	5	9	100.0	12	23	ABH83668	Oligonucleotide pr
c	6	9	100.0	12	23	ABH86802	Oligonucleotide pr
	7	9	100.0	12	23	ABH95571	Oligonucleotide pr
c	8	9	100.0	12	23	ABH99034	Oligonucleotide pr
	9	9	100.0	12	23	ABI06447	Oligonucleotide pr
	10	9	100.0	12	23	ABI14652	Oligonucleotide pr
	11	9	100.0	12	23	ABI16049	Oligonucleotide pr
c	12	9	100.0	12	23	ABI38611	Oligonucleotide pr
c	13	9	100.0	12	23	ABI39203	Oligonucleotide pr
	14	9	100.0	12	23	ABI40401	Oligonucleotide pr
c	15	9	100.0	12	23	ABI75163	Oligonucleotide pr
c	16	9	100.0	12	23	ABI76166	Oligonucleotide pr
	17	9	100.0	12	23	ABI78087	Oligonucleotide pr
c	18	9	100.0	12	23	ABI80232	Oligonucleotide pr
	19	9	100.0	13	23	ABC06168	Oligonucleotide SE
c	20	9	100.0	13	23	ABC06169	Oligonucleotide SE
	21	9	100.0	13	23	ABC20906	Oligonucleotide SE
c	22	9	100.0	13	23	ABC20907	Oligonucleotide SE
	23	9	100.0	13	23	ABC40316	Oligonucleotide SE
c	24	9	100.0	13	23	ABC40317	Oligonucleotide SE
	25	9	100.0	13	23	ABC54924	Oligonucleotide SE
c	26	9	100.0	13	23	ABC54925	Oligonucleotide SE
	27	9	100.0	13	23	ABC72172	Oligonucleotide SE
c	28	9	100.0	13	23	ABC72173	Oligonucleotide SE
	29	9	100.0	13	23	ABC84890	Oligonucleotide SE
c	30	9	100.0	13	23	ABC84891	Oligonucleotide SE
	31	9	100.0	13	23	ABF18052	Oligonucleotide SE
c	32	9	100.0	13	23	ABF18053	Oligonucleotide SE
	33	9	100.0	13	23	ABF28786	Oligonucleotide SE
c	34	9	100.0	13	23	ABF28787	Oligonucleotide SE
	35	9	100.0	13	23	ABF66366	Oligonucleotide SE
c	36	9	100.0	13	23	ABF66367	Oligonucleotide SE
	37	9	100.0	13	23	ABF92852	Oligonucleotide SE
c	38	9	100.0	13	23	ABF92853	Oligonucleotide SE
	39	9	100.0	13	23	ABH01812	Oligonucleotide SE
c	40	9	100.0	13	23	ABH01813	Oligonucleotide SE
	41	9	100.0	13	23	ABH16364	Oligonucleotide SE
c	42	9	100.0	13	23	ABH16365	Oligonucleotide SE
	43	9	100.0	13	23	ABH32012	Oligonucleotide SE
c	44	9	100.0	13	23	ABH32013	Oligonucleotide SE
	45	9	100.0	13	23	ABH40490	Oligonucleotide SE

ALIGNMENTS

RESULT 1
AAZ10693
ID AAZ10693 standard; DNA; 9 BP.
XX
AC AAZ10693;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 29; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 1 TAGGAGGAT 9

RESULT 2
AAS14906
ID AAS14906 standard; DNA; 9 BP.
XX
AC AAS14906;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #2.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #2, a scrambled
CC version of the oligonucleotide shown in AAS14905, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC described in the method of the invention.
XX
SQ Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 1 TAGGAGGAT 9

RESULT 3
ABH73149
ID ABH73149 standard; DNA; 12 BP.
XX
AC ABH73149;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 273134 for detecting SNP TSC0003058.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 273134; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed

```
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 other;

  Query Match           100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


RESULT 4
ABH79033/c
ID   ABH79033 standard; DNA; 12 BP.
XX
AC   ABH79033;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 279026 for detecting SNP TSC0006799.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 279026; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

  Query Match           100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         12 TAGGAGGAT 4


RESULT 5
ABH83668
ID   ABH83668 standard; DNA; 12 BP.
XX
AC   ABH83668;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 283661 for detecting SNP TSC0011446.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 283661; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 other;

  Query Match           100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


RESULT 6
ABH86802/c
ID   ABH86802 standard; DNA; 12 BP.
XX
AC   ABH86802;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 286795 for detecting SNP TSC0012825.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 286795; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 9 TAGGAGGAT 1

RESULT 7
ABH95571
ID ABH95571 standard; DNA; 12 BP.
XX
AC ABH95571;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 295564 for detecting SNP TSC0016640.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 295564; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 4 TAGGAGGAT 12

RESULT 8
ABH99034/c
ID ABH99034 standard; DNA; 12 BP.
XX
AC ABH99034;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299027 for detecting SNP TSC0018404.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 299027; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

```
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         12 TAGGAGGAT 4


RESULT 9
ABI06447
ID   ABI06447 standard; DNA; 12 BP.
XX
AC   ABI06447;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 306420 for detecting SNP TSC0022000.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 306420; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 10
ABI14652
ID   ABI14652 standard; DNA; 12 BP.
XX
AC   ABI14652;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 314625 for detecting SNP TSC0026468.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 314625; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;

  Query Match             100.0%;  Score 9;  DB 23;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          4 TAGGAGGAT 12


RESULT 11
ABI16049
ID   ABI16049 standard; DNA; 12 BP.
XX
```

AC ABI16049;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 316022 for detecting SNP TSC0027234.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 316022; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 2 TAGGAGGAT 10

RESULT 12
ABI38611/c
ID ABI38611 standard; DNA; 12 BP.
XX
AC ABI38611;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 338584 for detecting SNP TSC0040564.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 338584; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 12 TAGGAGGAT 4

RESULT 13
ABI39203/c
ID ABI39203 standard; DNA; 12 BP.
XX
AC ABI39203;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 339176 for detecting SNP TSC0040884.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 339176; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
||||||||| |
Db 12 TAGGAGGAT 4

RESULT 14
ABI40401
ID ABI40401 standard; DNA; 12 BP.
XX
AC ABI40401;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 340374 for detecting SNP TSC0041493.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 340374; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
||||||||| |
Db 1 TAGGAGGAT 9

RESULT 15
ABI75163/c
ID ABI75163 standard; DNA; 12 BP.
XX
AC ABI75163;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 375136 for detecting SNP TSC0061083.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 375136; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9

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                 |||||||||
Db          11 TAGGAGGAT 3
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Search completed: June 2, 2003, 18:45:10
Job time : 151.566 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:29:55 ; Search time 1129.39 Seconds
(without alignments)
129.060 Million cell updates/sec

Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	9	100.0	40	9	AA912717	AA912717 ol41a03.s
	3	8	88.9	19	17	AZ500675	AZ500675 1M0339J10
c	4	8	88.9	20	17	AZ393773	AZ393773 1M0157B04
c	5	8	88.9	21	17	AZ387199	AZ387199 1M0146P20
c	6	8	88.9	21	17	AZ645664	AZ645664 1M0511C13
	7	8	88.9	22	9	AI631347	AI631347 tz83c04.x
c	8	8	88.9	22	17	AZ411934	AZ411934 1M0185M09
c	9	8	88.9	23	17	AZ822831	AZ822831 2M0096J21
c	10	8	88.9	24	13	BG925475	BG925475 HNC5-1-C6
	11	8	88.9	24	17	AZ503909	AZ503909 1M0343E24
c	12	8	88.9	24	17	BH789331	BH789331 SALK_0190
	13	8	88.9	25	17	AZ491057	AZ491057 1M0324I24
	14	8	88.9	25	17	AZ496986	AZ496986 1M0333H09
c	15	8	88.9	28	17	AZ480483	AZ480483 1M0302J04
	16	8	88.9	28	17	AZ799431	AZ799431 2M0056I22
c	17	8	88.9	29	14	N22525	N22525 yw45e09.s1
c	18	8	88.9	29	17	AZ759923	AZ759923 1M0553I10
	19	8	88.9	29	17	TA6H12Q	AL451765 T. brucei
c	20	8	88.9	30	17	AZ312621	AZ312621 1M0028C18
c	21	8	88.9	30	17	AZ658025	AZ658025 1M0534N04
c	22	8	88.9	30	17	AZ817062	AZ817062 2M0086A12
c	23	8	88.9	31	9	AI583630	AI583630 tt74b05.x
	24	8	88.9	31	9	AA209595	AA209595 mw75d07.r
	25	8	88.9	31	17	AZ500072	AZ500072 1M0338A14
c	26	8	88.9	31	17	AZ663905	AZ663905 1M0543I17
	27	8	88.9	32	13	BJ059143	BJ059143 BJ059143
	28	8	88.9	32	17	AZ325144	AZ325144 1M0047J22
	29	8	88.9	33	17	AZ435186	AZ435186 1M0222E03
c	30	8	88.9	33	17	AZ486766	AZ486766 1M0315H10
c	31	8	88.9	33	17	BH856998	BH856998 SALK_0774
	32	8	88.9	34	17	BH814333	BH814333 SALK_0662
	33	8	88.9	35	14	H38132	H38132 yp46e11.r1
c	34	8	88.9	35	17	BH848385	BH848385 SALK_0680
c	35	8	88.9	36	13	BJ048452	BJ048452 BJ048452
c	36	8	88.9	36	14	T67214	T67214 ya53d11.r4
	37	8	88.9	37	9	AI629177	AI629177 fc04e06.y
c	38	8	88.9	37	17	BH023763	BH023763 BG02168-5
	39	8	88.9	37	17	BH850593	BH850593 SALK_0715
c	40	8	88.9	38	14	R37318	R37318 yf56b07.s1
	41	8	88.9	38	17	AZ802603	AZ802603 2M0061L06
	42	8	88.9	38	17	AZ818796	AZ818796 2M0089I06
c	43	8	88.9	38	17	AL758045	AL758045 Arabidops
	44	8	88.9	40	9	AA743356	AA743356 ny18c01.s
c	45	8	88.9	40	9	AI273000	AI273000 qv63e07.x

ALIGNMENTS

RESULT 1
AZ454138
LOCUS AZ454138 35 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0256A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0256A01 F, DNA sequence.
ACCESSION AZ454138
VERSION AZ454138.1 GI:10612263
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

```
          Plate: 0256  row: A  column: 01
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0256A01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      1 c      20 g      7 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 17;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          6 TAGGAGGAT 14


RESULT 2
AA912717
LOCUS       AA912717                 40 bp    mRNA    linear   EST 26-AUG-1998
DEFINITION  ol41a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1525996 3' similar to SW:BI3_MOUSE P28662 BRAIN PROTEIN I3 ;,
            mRNA sequence.
ACCESSION   AA912717
VERSION     AA912717.1  GI:3052109
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 449   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1525996"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT        8 a      10 c      10 g      12 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 9;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         24 TAGGAGGAT 32


RESULT 3
AZ500675
LOCUS       AZ500675                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0339J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0339J10 F, DNA sequence.
ACCESSION   AZ500675
VERSION     AZ500675.1  GI:10680728
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0339  row: J  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0339J10"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 0 c 9 g 6 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGA 8
||||||||
Db 11 TAGGAGGA 18

RESULT 4
AZ393773/c
LOCUS AZ393773 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0157B04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0157B04 F, DNA sequence.
ACCESSION AZ393773
VERSION AZ393773.1 GI:10508845
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: B column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0157B04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 11 c 1 g 6 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAGGAT 9
||||||||
Db 20 AGGAGGAT 13

RESULT 5
AZ387199/c
LOCUS AZ387199 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0146P20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0146P20 R, DNA sequence.
ACCESSION AZ387199
VERSION AZ387199.1 GI:10500900
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: P column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0146P20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 13 c 0 g 5 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGA 8
||||||||
Db 15 TAGGAGGA 8

RESULT 6
AZ645664/c
LOCUS AZ645664 21 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0511C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0511C13 F, DNA sequence.
ACCESSION AZ645664
VERSION AZ645664.1 GI:11775376
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511C13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 9 c 0 g 10 t
ORIGIN

Query Match 88.9%; Score 8; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGA 8
||||||||
Db 8 TAGGAGGA 1

RESULT 7
AI631347
LOCUS AI631347 22 bp mRNA linear EST 16-DEC-1999
DEFINITION tz83c04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2295174 3' similar to SW:PRP2_HUMAN P02812 SALIVARY PROLINE-RICH PROTEIN PRECURSOR ;contains element MER22 repetitive element ;, mRNA sequence.
ACCESSION AI631347
VERSION AI631347.1 GI:4682677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1010 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2295174"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
BASE COUNT 6 a 9 c 5 g 2 t
ORIGIN

```
  Query Match             88.9%;  Score 8;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGA 8
              ||||||||
Db         12 TAGGAGGA 19


RESULT 8
AZ411934/c
LOCUS       AZ411934                 22 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0185M09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0185M09 F, DNA sequence.
ACCESSION   AZ411934
VERSION     AZ411934.1  GI:10535947
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0185  row: M  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0185M09"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       2 a      8 c      5 g      7 t
ORIGIN
```

```
  Query Match             88.9%;  Score 8;  DB 17;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGGAGGAT 9
              ||||||||
Db          9 AGGAGGAT 2


RESULT 9
AZ822831/c
LOCUS       AZ822831                 23 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0096J21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0096J21 F, DNA sequence.
ACCESSION   AZ822831
VERSION     AZ822831.1  GI:12992739
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0096  row: J  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0096J21"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       7 a      5 c      6 g      5 t
ORIGIN
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  Query Match             88.9%;  Score 8;  DB 17;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGA 8
              ||||||||
Db         14 TAGGAGGA 7


RESULT 10
BG925475/c
LOCUS       BG925475                 24 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC5-1-C6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG925475
VERSION     BG925475.1  GI:14319998
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"
BASE COUNT        4 a      9 c      1 g     10 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 13;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGGAGGAT 9
              ||||||||
Db         11 AGGAGGAT 4


RESULT 11
AZ503909
LOCUS       AZ503909                 24 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0343E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0343E24 R, DNA sequence.
ACCESSION   AZ503909
VERSION     AZ503909.1  GI:10685225
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0343  row: E  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0343E24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        4 a      3 c      9 g      8 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGA 8
              ||||||||
Db          7 TAGGAGGA 14


RESULT 12
BH789331/c
LOCUS       BH789331                 24 bp    DNA     linear   GSS 02-APR-2002
DEFINITION  SALK_019058.23.05.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_019058.23.05.x, DNA
            sequence.
ACCESSION   BH789331
VERSION     BH789331.1  GI:19882429
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
```

```
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_019058.23.05.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT        2 a      14 c       0 g       8 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGGAGGAT 9
              ||||||||
Db          8 AGGAGGAT 1


RESULT 13
AZ491057
LOCUS       AZ491057                  25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0324I24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0324I24 F, DNA sequence.
ACCESSION   AZ491057
VERSION     AZ491057.1  GI:10662392
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0324  row: I  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0324I24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      4 c      12 g      2 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGGAGGAT 9
              ||||||||
Db          9 AGGAGGAT 16


RESULT 14
AZ496986
LOCUS       AZ496986                  25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0333H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0333H09 R, DNA sequence.
ACCESSION   AZ496986
VERSION     AZ496986.1  GI:10673556
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0333  row: H  column: 09
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          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0333H09"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a      1 c      10 g      2 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGA 8
              ||||||||
Db         17 TAGGAGGA 24


RESULT 15
AZ480483/c
LOCUS       AZ480483                  28 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0302J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0302J04 F, DNA sequence.
ACCESSION   AZ480483
VERSION     AZ480483.1  GI:10641548
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from.10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0302  row: J  column: 04
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          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0302J04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       4 a      11 c      6 g      7 t
ORIGIN

  Query Match             88.9%;  Score 8;  DB 17;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGA 8
              ||||||||
Db         13 TAGGAGGA 6


Search completed: June  2, 2003, 20:35:37
Job time : 1133.39 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:31:20 ; Search time 36.878 Seconds
(without alignments)
74.844 Million cell updates/sec

Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	3	US-09-048-927-2	Sequence 2, Appli
	2	9	100.0	20	4	US-09-096-172-6	Sequence 6, Appli
	3	9	100.0	22	4	US-09-240-918-9	Sequence 9, Appli
c	4	9	100.0	24	4	US-09-416-050A-15	Sequence 15, Appl
c	5	9	100.0	24	4	US-09-664-800-15	Sequence 15, Appl
c	6	9	100.0	24	4	US-09-665-309-15	Sequence 15, Appl
c	7	9	100.0	24	4	US-09-661-569-15	Sequence 15, Appl
	8	9	100.0	28	4	US-09-061-768A-33	Sequence 33, Appl
c	9	9	100.0	29	1	US-08-310-356-20	Sequence 20, Appl
c	10	9	100.0	30	4	US-09-019-793A-105	Sequence 105, App
c	11	9	100.0	33	2	US-08-189-256A-46	Sequence 46, Appl
c	12	9	100.0	33	4	US-09-193-853-46	Sequence 46, Appl
	13	9	100.0	36	5	PCT-US95-00605-12	Sequence 12, Appl
	14	9	100.0	36	5	PCT-US95-00605-13	Sequence 13, Appl
	15	8	88.9	12	3	US-09-290-449-15	Sequence 15, Appl
c	16	8	88.9	15	1	US-08-182-968A-168	Sequence 168, App
c	17	8	88.9	15	1	US-08-182-968A-169	Sequence 169, App
c	18	8	88.9	15	2	US-08-774-306A-168	Sequence 168, App
c	19	8	88.9	15	2	US-08-774-306A-169	Sequence 169, App
	20	8	88.9	15	3	US-09-105-515-4	Sequence 4, Appli
c	21	8	88.9	15	3	US-09-064-156A-168	Sequence 168, App
c	22	8	88.9	15	3	US-09-064-156A-169	Sequence 169, App
	23	8	88.9	15	4	US-09-748-044-4	Sequence 4, Appli
	24	8	88.9	16	1	US-07-664-989B-100	Sequence 100, App
c	25	8	88.9	16	1	US-07-664-989B-101	Sequence 101, App
	26	8	88.9	16	2	US-08-282-197C-20	Sequence 20, Appl
	27	8	88.9	17	1	US-08-184-422-4	Sequence 4, Appli
c	28	8	88.9	17	1	US-08-758-306-1307	Sequence 1307, Ap
c	29	8	88.9	17	1	US-08-758-306-1309	Sequence 1309, Ap
c	30	8	88.9	17	1	US-08-758-306-1311	Sequence 1311, Ap
	31	8	88.9	17	3	US-08-589-771B-4	Sequence 4, Appli
c	32	8	88.9	17	3	US-08-606-505B-45	Sequence 45, Appl
c	33	8	88.9	17	4	US-09-616-990-45	Sequence 45, Appl
	34	8	88.9	17	4	US-08-584-040-1958	Sequence 1958, Ap
c	35	8	88.9	18	1	US-08-135-511-12	Sequence 12, Appl
c	36	8	88.9	18	1	US-08-319-492B-735	Sequence 735, App
	37	8	88.9	18	1	US-08-320-559-9	Sequence 9, Appli
	38	8	88.9	18	1	US-08-327-392-9	Sequence 9, Appli
c	39	8	88.9	18	1	US-08-187-453-12	Sequence 12, Appl
c	40	8	88.9	18	1	US-08-758-306-1379	Sequence 1379, Ap
c	41	8	88.9	18	1	US-08-207-412B-7	Sequence 7, Appli
	42	8	88.9	18	3	US-08-545-860D-9	Sequence 9, Appli
	43	8	88.9	18	3	US-08-912-272-87	Sequence 87, Appl
	44	8	88.9	18	4	US-09-050-159-26	Sequence 26, Appl
c	45	8	88.9	18	4	US-09-071-433-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-048-927-2
; Sequence 2, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-2

Query Match 100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9
```

RESULT 2
US-09-096-172-6
; Sequence 6, Application US/09096172
; Patent No. 6284252
; GENERAL INFORMATION:
; APPLICANT: MEHTALI, Majid
; APPLICANT: SORG, Tania
; TITLE OF INVENTION: NEW TRANSDOMINANT TAT VARIANTS OF THE
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia

```
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/096,172
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/177,145
;       FILING DATE:  04-JAN-1994
;       APPLICATION NUMBER:  FR 93 00004
;       FILING DATE:  04-JAN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane-Feury, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  017753-040
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  mutagenesis oligonucleotide (TAT
;       INDIVIDUAL ISOLATE:  45Ile to Ser)
US-09-096-172-6

  Query Match             100.0%;  Score 9;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          5 TAGGAGGAT 13


RESULT 3
US-09-240-918-9
; Sequence 9, Application US/09240918
; Patent No. 6265165
; GENERAL INFORMATION:
;  APPLICANT: Gruenert, Dieter C.
;  APPLICANT:  Xu, Zhidong
;  TITLE OF INVENTION: METHODS FOR EST-SPECIFIC FULL LENGTH cDNA CLONING
;  FILE REFERENCE: 480.85.1(HV)
;  CURRENT APPLICATION NUMBER: US/09/240,918
;  CURRENT FILING DATE:  1999-01-29
;  PRIOR APPLICATION NUMBER: 60/108,183
;  PRIOR FILING DATE: 1998-11-12
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-240-918-9

  Query Match             100.0%;  Score 9;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          9 TAGGAGGAT 17


RESULT 4
US-09-416-050A-15/c
; Sequence 15, Application US/09416050A
; Patent No. 6194559
; GENERAL INFORMATION:
;  APPLICANT:  KIM. Soo Young
;  TITLE OF INVENTION:  Abscisic Acid Responsive Element -Binding Transcription Facto
;  FILE REFERENCE:  1942/42
;  CURRENT APPLICATION NUMBER: US/09/416,050A
;  CURRENT FILING DATE:  1999-10-12
;  NUMBER OF SEQ ID NOS:  83
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-416-050A-15

  Query Match             100.0%;  Score 9;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 5
US-09-664-800-15/c
; Sequence 15, Application US/09664800
; Patent No. 6218527
; GENERAL INFORMATION:
;  APPLICANT:    KIM. Soo Young
;  TITLE OF INVENTION:    Abscisic Acid Responsive Element -Binding Transcription Fac
;  FILE REFERENCE:   1942/42
;  CURRENT APPLICATION NUMBER: US/09/664,800
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER:   09/416,050
;  PRIOR FILING DATE:   1999-10-12
;  NUMBER OF SEQ ID NOS:    83
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-664-800-15

  Query Match             100.0%;  Score 9;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 6
US-09-665-309-15/c
; Sequence 15, Application US/09665309
; Patent No. 6232461
; GENERAL INFORMATION:
;  APPLICANT:    KIM. Soo Young
;  TITLE OF INVENTION:    Abscisic Acid Responsive Element -Binding Transcription Fac
;  FILE REFERENCE:   1942/42
;  CURRENT APPLICATION NUMBER: US/09/665,309
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER:   09/416,050
;  PRIOR FILING DATE:   1999-10-12
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;  NUMBER OF SEQ ID NOS:    83
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-665-309-15

  Query Match             100.0%;  Score 9;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 7
US-09-661-569-15/c
; Sequence 15, Application US/09661569
; Patent No. 6245905
; GENERAL INFORMATION:
;  APPLICANT:    KIM. Soo Young
;  TITLE OF INVENTION:    Abscisic Acid Responsive Element -Binding Transcription Factor
;  FILE REFERENCE:   1942/42
;  CURRENT APPLICATION NUMBER: US/09/661,569
;  CURRENT FILING DATE:  2000-09-14
;  PRIOR APPLICATION NUMBER:   09/416,050
;  PRIOR FILING DATE:   1999-10-12
;  NUMBER OF SEQ ID NOS:    83
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-661-569-15

  Query Match             100.0%;  Score 9;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 8
US-09-061-768A-33
; Sequence 33, Application US/09061768A
; Patent No. 6204037
;  GENERAL INFORMATION:
;    APPLICANT:  BRASH, ALAN R.
;    APPLICANT:  BOEGLIN, WILLIAM E.
;    APPLICANT:  JISAKA, MITSUO
;    TITLE OF INVENTION:  LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARLES A. TAYLOR, JR.
;      STREET:  SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
;      CITY:  DURHAM
;      STATE:  NORTH CAROLINA
;      COUNTRY:  USA
;      ZIP:  27707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 MB storage
;      COMPUTER:  IBM PC/XT/AT compatible
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  WORD PERFECT 6.1 and ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/061,768A
;      FILING DATE:  APRIL 16, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:  NONE
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ARLES A. TAYLOR, JR.
;      REGISTRATION NUMBER:  39,395
;      REFERENCE/DOCKET NUMBER:  1242/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 493-8000
;      TELEFAX:  (919) 419-0383
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-061-768A-33

  Query Match             100.0%;  Score 9;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          7 TAGGAGGAT 15


RESULT 9
US-08-310-356-20/c
; Sequence 20, Application US/08310356
; Patent No. 5648243
;  GENERAL INFORMATION:
;    APPLICANT:  Hurwitz, David R
;    APPLICANT:  Nathan, Margret
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  Transgenic Protein Production
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Legal Department
;      STREET:  500 Arcola Road
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System 7.0
;      SOFTWARE:  Microsoft Word Version 5.0 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,356
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,853
;      FILING DATE:  31-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goodman, Rosanne
;      REGISTRATION NUMBER:  32,534
;      REFERENCE/DOCKET NUMBER:  A0856
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 454-3817
;      TELEFAX:  (215) 454-3808
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-310-356-20

  Query Match             100.0%;  Score 9;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
```

```
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         23 TAGGAGGAT 15


RESULT 10
US-09-019-793A-105/c
; Sequence 105, Application US/09019793A
; Patent No. 6380376
; GENERAL INFORMATION:
;  APPLICANT:  PAUL, Prem
;  APPLICANT:  MENG, Xiang-Jin
;  APPLICANT:  MOROZOV, Igor
;  APPLICANT:  HALBUR, Patrick
;  TITLE OF INVENTION:  PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
;  TITLE OF INVENTION:  REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV)
;  FILE REFERENCE:  4625-0039-55X CIP
;  CURRENT APPLICATION NUMBER: US/09/019,793A
;  CURRENT FILING DATE:  1998-02-06
;  PRIOR APPLICATION NUMBER:  08/478,316
;  PRIOR FILING DATE:  1995-06-07
;  PRIOR APPLICATION NUMBER:  08/301,435
;  PRIOR FILING DATE:  1994-09-01
;  PRIOR APPLICATION NUMBER:  08/131,625
;  PRIOR FILING DATE:  1993-10-05
;  PRIOR APPLICATION NUMBER:  07/969,071
;  PRIOR FILING DATE:  1992-10-30
;  NUMBER OF SEQ ID NOS:  108
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-09-019-793A-105

  Query Match             100.0%;  Score 9;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         15 TAGGAGGAT 7


RESULT 11
US-08-189-256A-46/c
; Sequence 46, Application US/08189256A
; Patent No. 5877402
;  GENERAL INFORMATION:
;    APPLICANT:  Maliga, Pal
;    APPLICANT:  Svab, Zora
;    APPLICANT:  Staub, Jeffrey
;    APPLICANT:  Zoubenko, Oleg V.
;    APPLICANT:  Allison, Lori A.
;    APPLICANT:  Carrer, Helaine
;    APPLICANT:  Kanevski, Ivan
;    TITLE OF INVENTION:  DNA Constructs and Methods for Stably
;    TITLE OF INVENTION:  Transforming Plastids of Multicellular Plants and
;    TITLE OF INVENTION:  Expressing Recombinant Proteins Therein
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dann, Dorfman, Herrell and Skillman
;      STREET:  1601 Market Street  Suite 720
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-2307
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/189,256A
;      FILING DATE:  31-JAN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/111,398
;      FILING DATE:  25-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US o7/518,763
;      FILING DATE:  01-MAY-1990
;    ATTORNEY/AGENT INEORMATION:
;      NAME:  Reed, Janet E.
;      REGISTRATION NUMBER:  36,252
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-4100
;      TELEFAX:  (215) 563-4044
;  INFORMATION FOR SEQ ID NO:  46:
;   SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-189-256A-46

  Query Match             100.0%;  Score 9;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         27 TAGGAGGAT 19


RESULT 12
US-09-193-853-46/c
; Sequence 46, Application US/09193853
; Patent No. 6388168
;  GENERAL INFORMATION:
;    APPLICANT:  Maliga, Pal
;    APPLICANT:  Svab, Zora
;    APPLICANT:  Staub, Jeffrey
;    APPLICANT:  Zoubenko, Oleg V.
;    APPLICANT:  Allison, Lori A.
;    APPLICANT:  Carrer, Helaine
;    APPLICANT:  Kanevski, Ivan
;    TITLE OF INVENTION:  DNA Constructs and Methods for Stably
;    TITLE OF INVENTION:  Transforming Plastids of Multicellular Plants and
;    TITLE OF INVENTION:  Expressing Recombinant Proteins Therein
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dann, Dorfman, Herrell and Skillman
;      STREET:  1601 Market Street  Suite 720
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-2307
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/193,853
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/189,256
```

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;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US o7/518,763
;       FILING DATE:  01-MAY-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Reed, Janet E.
;       REGISTRATION NUMBER:  36,252
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-4100
;       TELEFAX:  (215) 563-4044
;   INFORMATION FOR SEQ ID NO:  46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  33 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-09-193-853-46

  Query Match             100.0%;  Score 9;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         27 TAGGAGGAT 19


RESULT 13
PCT-US95-00605-12
; Sequence 12, Application PC/TUS9500605
;  GENERAL INFORMATION:
;    APPLICANT:  Lyle, Leon
;    APPLICANT:  Thomas-Miller, Beth
;    TITLE OF INVENTION:  THERAPEUTIC TREATMENT FOR INHIBITING
;    TITLE OF INVENTION:  VASCULAR RESTENOSIS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mallinckrodt Medical, Inc.
;      STREET:  675 McDonnell Boulevard, P.O. Box 5840
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63134
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00605
;      FILING DATE:  13-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/182,917
;      FILING DATE:  14-JAN-1994
;      APPLICATION NUMBER:  US 07/965,678
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vacca, Rita D.
;      REGISTRATION NUMBER:  33,624
;      REFERENCE/DOCKET NUMBER:  0783.2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  314-895-7215
;      TELEFAX:  314-895-2156
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
;    ORIGINAL SOURCE:
;      ORGANISM:  Macrophage Inflammatory Protein-1 Beta
;      STRAIN:  human
PCT-US95-00605-12

  Query Match             100.0%;  Score 9;  DB 5;  Length 36;
  Best Local Similarity   77.8%;  Pred. No. 2e+03;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              :|||||||:
Db          2 UAGGAGGAU 10


RESULT 14
PCT-US95-00605-13
; Sequence 13, Application PC/TUS9500605
;  GENERAL INFORMATION:
;    APPLICANT:  Lyle, Leon
;    APPLICANT:  Thomas-Miller, Beth
;    TITLE OF INVENTION:  THERAPEUTIC TREATMENT FOR INHIBITING
;    TITLE OF INVENTION:  VASCULAR RESTENOSIS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mallinckrodt Medical, Inc.
;      STREET:  675 McDonnell Boulevard, P.O. Box 5840
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63134
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00605
;      FILING DATE:  13-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/182,917
;      FILING DATE:  14-JAN-1994
;      APPLICATION NUMBER:  US 07/965,678
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vacca, Rita D.
;      REGISTRATION NUMBER:  33,624
;      REFERENCE/DOCKET NUMBER:  0783.2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  314-895-7215
;      TELEFAX:  314-895-2156
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
;    ORIGINAL SOURCE:
;      ORGANISM:  Macrophage Inflammatory Protein-1 Beta
;      STRAIN:  human
PCT-US95-00605-13

  Query Match             100.0%;  Score 9;  DB 5;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
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```
              |||||||||
Db          2 TAGGAGGAT 10


RESULT 15
US-09-290-449-15
; Sequence 15, Application US/09290449A
; Patent No. 6096505
; GENERAL INFORMATION:
;  APPLICANT: SELBY, Mark
;  APPLICANT: THUDIUM, Kent
;  APPLICANT: DINA, Dino
;  TITLE OF INVENTION: NONCLONING TECHNIQUE FOR EXPRESSING A GENE OF INTEREST
;  FILE REFERENCE: 1448.002
;  CURRENT APPLICATION NUMBER: US/09/290,449A
;  CURRENT FILING DATE: 1999-04-13
;  EARLIER APPLICATION NUMBER: US 60/081,777
;  EARLIER FILING DATE: 1998-04-14
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(12)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Flexible Hinge
;   OTHER INFORMATION: Sequence (Fig. 1)
; Patent No. 6096505
US-09-290-449-15

  Query Match             88.9%;  Score 8;  DB 3;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGGAGGAT 9
              ||||||||
Db          3 AGGAGGAT 10


Search completed: June  2, 2003, 20:38:32
Job time : 37.878 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 19:09:45 ; Search time 63.878 Seconds
(without alignments)
189.976 Million cell updates/sec

Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 477662

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	9	US-10-122-630-2	Sequence 2, Appli
	2	9	100.0	9	9	US-10-122-633-2	Sequence 2, Appli
	3	9	100.0	20	9	US-09-828-344-162	Sequence 162, App
	4	9	100.0	20	9	US-09-828-344-163	Sequence 163, App
	5	9	100.0	20	9	US-09-828-344-164	Sequence 164, App
	6	9	100.0	20	10	US-09-766-154-19	Sequence 19, Appl
c	7	9	100.0	21	9	US-09-816-814-13	Sequence 13, Appl
	8	9	100.0	26	9	US-09-949-427-202	Sequence 202, App
	9	9	100.0	28	10	US-09-764-246-33	Sequence 33, Appl
c	10	9	100.0	30	9	US-10-104-019-105	Sequence 105, App
c	11	9	100.0	31	9	US-09-912-263-64	Sequence 64, Appl
c	12	9	100.0	36	9	US-10-011-672-5	Sequence 5, Appli
c	13	9	100.0	36	9	US-10-012-013-5	Sequence 5, Appli
c	14	9	100.0	36	9	US-10-012-070A-5	Sequence 5, Appli
	15	8	88.9	10	9	US-10-055-713-67	Sequence 67, Appl
	16	8	88.9	10	9	US-09-990-186-1611	Sequence 1611, Ap
	17	8	88.9	10	10	US-09-989-789-1611	Sequence 1611, Ap
	18	8	88.9	15	9	US-10-287-919-1170	Sequence 1170, Ap
	19	8	88.9	15	9	US-10-287-919-1205	Sequence 1205, Ap
c	20	8	88.9	15	10	US-09-504-231A-190	Sequence 190, App
c	21	8	88.9	15	10	US-09-504-231A-191	Sequence 191, App
c	22	8	88.9	15	10	US-09-274-553D-190	Sequence 190, App
c	23	8	88.9	15	10	US-09-274-553D-191	Sequence 191, App
	24	8	88.9	16	9	US-10-287-919-1008	Sequence 1008, Ap
	25	8	88.9	16	9	US-10-287-919-1009	Sequence 1009, Ap
	26	8	88.9	16	10	US-09-781-988-100	Sequence 100, App
c	27	8	88.9	16	10	US-09-781-988-101	Sequence 101, App
	28	8	88.9	17	9	US-10-060-830-246	Sequence 246, App
	29	8	88.9	17	9	US-10-060-830-247	Sequence 247, App
	30	8	88.9	17	9	US-10-060-830-248	Sequence 248, App
	31	8	88.9	17	9	US-10-060-830-249	Sequence 249, App
	32	8	88.9	17	9	US-10-060-830-250	Sequence 250, App
	33	8	88.9	17	9	US-10-060-830-251	Sequence 251, App
	34	8	88.9	17	9	US-10-060-830-252	Sequence 252, App
	35	8	88.9	17	9	US-10-060-830-253	Sequence 253, App
	36	8	88.9	17	9	US-10-060-830-254	Sequence 254, App
	37	8	88.9	17	9	US-10-060-830-255	Sequence 255, App
	38	8	88.9	17	9	US-09-780-164-26	Sequence 26, Appl
	39	8	88.9	17	9	US-09-780-164-394	Sequence 394, App
	40	8	88.9	17	9	US-09-780-164-760	Sequence 760, App
	41	8	88.9	17	9	US-09-780-164-859	Sequence 859, App
	42	8	88.9	17	9	US-09-780-164-967	Sequence 967, App
	43	8	88.9	17	9	US-09-780-164-968	Sequence 968, App
	44	8	88.9	17	9	US-09-780-164-969	Sequence 969, App
	45	8	88.9	17	9	US-09-780-164-970	Sequence 970, App

ALIGNMENTS

RESULT 1
US-10-122-630-2
; Sequence 2, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-2

Query Match 100.0%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
|||||||||
Db 1 TAGGAGGAT 9

```
RESULT 2
US-10-122-633-2
; Sequence 2, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-2

  Query Match             100.0%;  Score 9;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+08;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 3
US-09-828-344-162
; Sequence 162, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTS-0147
;  CURRENT APPLICATION NUMBER: US/09/828,344
;  CURRENT FILING DATE:  2001-04-06
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 162
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-162

  Query Match             100.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 4
US-09-828-344-163
; Sequence 163, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTS-0147
;  CURRENT APPLICATION NUMBER: US/09/828,344
;  CURRENT FILING DATE:  2001-04-06
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 163
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-163

  Query Match             100.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


RESULT 5
US-09-828-344-164
; Sequence 164, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTS-0147
;  CURRENT APPLICATION NUMBER: US/09/828,344
;  CURRENT FILING DATE:  2001-04-06
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 164
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-164

  Query Match             100.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          4 TAGGAGGAT 12


RESULT 6
US-09-766-154-19
; Sequence 19, Application US/09766154
; Patent No. US20020010948A1
; GENERAL INFORMATION:
;  APPLICANT:  Patience, Clive
;  TITLE OF INVENTION:  Swine Defective for Transmission of Porcine Endogenous
;  TITLE OF INVENTION:  Retrovirus and Uses Thereof
;  FILE REFERENCE:  61750-311
;  CURRENT APPLICATION NUMBER: US/09/766,154
;  CURRENT FILING DATE:  2001-01-19
;  PRIOR APPLICATION NUMBER:  U.S. 60/243695
;  PRIOR FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  U.S. 60/182965
;  PRIOR FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER:  U.S. 60/177003
;  PRIOR FILING DATE:  2000-01-19
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   OTHER INFORMATION: sequence used in amplification of PERV-sequences.
US-09-766-154-19

  Query Match             100.0%;  Score 9;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          2 TAGGAGGAT 10


RESULT 7
US-09-816-814-13/c
; Sequence 13, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
;  APPLICANT: Goronzy, Jorg J.
;  APPLICANT:  Weyand, Cornelia M.
;  TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
;  FILE REFERENCE: 07039-251001
;  CURRENT APPLICATION NUMBER: US/09/816,814
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer for PCR
US-09-816-814-13

  Query Match             100.0%;  Score 9;  DB 9;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         15 TAGGAGGAT 7


RESULT 8
US-09-949-427-202
; Sequence 202, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
;  FILE REFERENCE: 02810.0014.NPUS02
;  CURRENT APPLICATION NUMBER: US/09/949,427
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-427-202

  Query Match             100.0%;  Score 9;  DB 9;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          6 TAGGAGGAT 14


RESULT 9
US-09-764-246-33
; Sequence 33, Application US/09764246
; Patent No. US20010046672A1
;   GENERAL INFORMATION:
;        APPLICANT: BRASH, ALAN R.
;                   BOEGLIN, WILLIAM E.
;                   JISAKA, MITSUO
;        TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ARLES A. TAYLOR, JR.
;             STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
;             CITY: DURHAM
;             STATE: NORTH CAROLINA
;             COUNTRY: USA
;             ZIP: 27707
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
;             COMPUTER: IBM PC/XT/AT compatible
;             OPERATING SYSTEM: Windows 3.1
;             SOFTWARE: WORD PERFECT 6.1 and ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/764,246
;             FILING DATE: 17-Jan-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: ARLES A. TAYLOR, JR.
;             REGISTRATION NUMBER: 39,395
;             REFERENCE/DOCKET NUMBER: 1242/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919) 493-8000
;             TELEFAX: (919) 419-0383
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 33:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 28 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-764-246-33

  Query Match             100.0%;  Score 9;  DB 10;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          7 TAGGAGGAT 15


RESULT 10
US-10-104-019-105/c
; Sequence 105, Application US/10104019
; Patent No. US20020168379A1
; GENERAL INFORMATION:
;  APPLICANT: PAUL, Prem
;  APPLICANT:  MENG, Xiang-Jin
;  APPLICANT:  MOROZOV, Igor
```

```
;  APPLICANT:  HALBUR, Patrick
;  TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
;  TITLE OF INVENTION:  REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV)
;  FILE REFERENCE: 4625-0039-55X CIP
;  CURRENT APPLICATION NUMBER: US/10/104,019
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: 09/019,793
;  PRIOR FILING DATE: 1998-02-06
;  PRIOR APPLICATION NUMBER: 08/301,435
;  PRIOR FILING DATE: 1994-09-01
;  PRIOR APPLICATION NUMBER: 08/131,625
;  PRIOR FILING DATE: 1993-10-05
;  PRIOR APPLICATION NUMBER: 07/969,071
;  PRIOR FILING DATE: 1992-10-30
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-10-104-019-105

  Query Match             100.0%;  Score 9;  DB 9;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         15 TAGGAGGAT 7


RESULT 11
US-09-912-263-64/c
; Sequence 64, Application US/09912263
; Publication No. US20030039973A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric. S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2017-001
;  CURRENT APPLICATION NUMBER: US/09/912,263
;  CURRENT FILING DATE:  2001-07-24
;  PRIOR APPLICATION NUMBER: US 60/220,315
;  PRIOR FILING DATE: 2000-07-24
;  NUMBER OF SEQ ID NOS: 552
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-912-263-64

  Query Match             100.0%;  Score 9;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         31 TAGGAGGAT 23


RESULT 12
US-10-011-672-5/c
; Sequence 5, Application US/10011672
; Publication No. US20030049814A1
; GENERAL INFORMATION:
;  APPLICANT: Hawkes, Timothy
;  APPLICANT:  Warner, Simon
;  APPLICANT:  Andrews, Christopher
;  APPLICANT:  Bachoo, Satvinder
;  APPLICANT:  Pickerill, Andrew
;  TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
;  FILE REFERENCE: 50489/UST
;  CURRENT APPLICATION NUMBER: US/10/011,672
;  CURRENT FILING DATE:  2001-10-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/01559
;  PRIOR FILING DATE: 2000-04-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-10-011-672-5

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Qy          1 TAGGAGGAT 9
              |||||||||
Db         26 TAGGAGGAT 18


RESULT 13
US-10-012-013-5/c
; Sequence 5, Application US/10012013
; Publication No. US20030079246A1
; GENERAL INFORMATION:
;  APPLICANT: Hawkes, Timothy
;  APPLICANT:  Warner, Simon
;  APPLICANT:  Andrews, Christopher
;  APPLICANT:  Bachoo, Satvinder
;  APPLICANT:  Pickerill, Andrew
;  TITLE OF INVENTION: Herbicide Resistant Plants
;  FILE REFERENCE: 50450/UST
;  CURRENT APPLICATION NUMBER: US/10/012,013
;  CURRENT FILING DATE:  2001-10-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/01572
;  PRIOR FILING DATE: 2000-04-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-013-5

  Query Match             100.0%;  Score 9;  DB 9;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         26 TAGGAGGAT 18


RESULT 14
US-10-012-070A-5/c
; Sequence 5, Application US/10012070A
; Publication No. US20030077801A1
; GENERAL INFORMATION:
;  APPLICANT: Hawkes, Timothy
;  APPLICANT:  Warner, Simon
;  APPLICANT:  Andrews, Christopher
;  APPLICANT:  Bachoo, Satvinder
;  APPLICANT:  Pickerill, Andrew
;  TITLE OF INVENTION: Herbicide Resistant Plants
;  FILE REFERENCE: 50490/UST
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; CURRENT APPLICATION NUMBER: US/10/012,070A
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-5

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TAGGAGGAT 9
              |||||||||
Db         26 TAGGAGGAT 18
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RESULT 15
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; Sequence 67, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; TITLE OF INVENTION: REGULATION IN PLANTS
; FILE REFERENCE: 8325-0026 / S26-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 9 target sequence
US-10-055-713-67

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Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          2 AGGAGGAT 9
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 11746948

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	9	100.0	9	21	US-09-540-843-2	Sequence 2, Appli
	2	9	100.0	9	40	US-10-122-630-2	Sequence 2, Appli
	3	9	100.0	9	40	US-10-122-633-2	Sequence 2, Appli
	4	9	100.0	10	42	US-10-223-765-202	Sequence 202, App
c	5	9	100.0	16	33	US-09-882-945A-169	Sequence 169, App
	6	9	100.0	18	65	US-60-216-745-6947	Sequence 6947, Ap
	7	9	100.0	18	65	US-60-216-745-11899	Sequence 11899, A
c	8	9	100.0	19	1	PCT-US00-25479-22	Sequence 22, Appl
	9	9	100.0	19	1	PCT-US00-25479-76	Sequence 76, Appl
c	10	9	100.0	19	17	US-09-398-522-22	Sequence 22, Appl
	11	9	100.0	19	17	US-09-398-522-76	Sequence 76, Appl
	12	9	100.0	19	65	US-60-216-745-8613	Sequence 8613, Ap
	13	9	100.0	20	1	PCT-US01-01857-19	Sequence 19, Appl
	14	9	100.0	20	1	PCT-US02-10529-162	Sequence 162, App
	15	9	100.0	20	1	PCT-US02-10529-163	Sequence 163, App
	16	9	100.0	20	1	PCT-US02-10529-164	Sequence 164, App
c	17	9	100.0	20	1	PCT-US02-12063-200	Sequence 200, App
	18	9	100.0	20	5	US-08-177-145-6	Sequence 6, Appli
c	19	9	100.0	20	16	US-09-201-228A-2181	Sequence 2181, Ap
c	20	9	100.0	20	16	US-09-201-228A-3736	Sequence 3736, Ap
c	21	9	100.0	20	18	US-09-422-978-6304	Sequence 6304, Ap

	22	9	100.0	20	30	US-09-766-154-19	Sequence 19, Appl
	23	9	100.0	20	31	US-09-828-344-162	Sequence 162, App
	24	9	100.0	20	31	US-09-828-344-163	Sequence 163, App
	25	9	100.0	20	31	US-09-828-344-164	Sequence 164, App
	26	9	100.0	20	38	US-10-006-191-104	Sequence 104, App
c	27	9	100.0	20	40	US-10-126-022-200	Sequence 200, App
c	28	9	100.0	21	18	US-09-422-978-9775	Sequence 9775, Ap
c	29	9	100.0	21	31	US-09-816-814-13	Sequence 13, Appl
	30	9	100.0	22	3	US-07-598-420-16	Sequence 16, Appl
c	31	9	100.0	23	1	PCT-US97-02396-33	Sequence 33, Appl
c	32	9	100.0	23	8	US-08-472-801-1428	Sequence 1428, Ap
c	33	9	100.0	23	10	US-08-668-235-1428	Sequence 1428, Ap
c	34	9	100.0	23	24	US-09-634-306B-68219	Sequence 68219, A
c	35	9	100.0	23	38	US-10-027-632-68219	Sequence 68219, A
	36	9	100.0	23	80	US-60-361-523-12	Sequence 12, Appl
c	37	9	100.0	23	80	US-60-361-523-13	Sequence 13, Appl
	38	9	100.0	24	1	PCT-US00-20638-318	Sequence 318, App
c	39	9	100.0	25	17	US-09-396-196F-27690	Sequence 27690, A
c	40	9	100.0	25	17	US-09-396-196F-27691	Sequence 27691, A
c	41	9	100.0	25	17	US-09-396-196F-53922	Sequence 53922, A
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c	43	9	100.0	25	17	US-09-396-196F-94038	Sequence 94038, A
c	44	9	100.0	25	17	US-09-396-196F-98060	Sequence 98060, A
c	45	9	100.0	25	17	US-09-396-196F-98061	Sequence 98061, A

ALIGNMENTS

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RESULT 1
US-09-540-843-2
; Sequence 2, Application US/09540843
; GENERAL INFORMATION:
;  APPLICANT:  Gilchrest, Barbara A.
;  APPLICANT:  Yaar, Mina
;  APPLICANT:  Eller, Mark
;  TITLE OF INVENTION:  USE OF LOCALLY APPLIED DNA FRAGMENTS
;  FILE REFERENCE:  0054.1088-015
;  CURRENT APPLICATION NUMBER: US/09/540,843
;  CURRENT FILING DATE:  2000-03-31
;  PRIOR APPLICATION NUMBER:  US 09/048,927
;  PRIOR FILING DATE:  1998-03-26
;  PRIOR APPLICATION NUMBER:  US 08/952,697
;  PRIOR FILING DATE:  1996-06-03
;  PRIOR APPLICATION NUMBER:  US 08/467,012
;  PRIOR FILING DATE:  1995-06-06
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-09-540-843-2

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  Best Local Similarity   100.0%;  Pred. No. 2.8e+09;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 2
US-10-122-630-2
; Sequence 2, Application US/10122630
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-2

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  Best Local Similarity   100.0%;  Pred. No. 2.8e+09;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 3
US-10-122-633-2
; Sequence 2, Application US/10122633
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-2

  Query Match             100.0%;  Score 9;  DB 40;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+09;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
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Db          1 TAGGAGGAT 9


RESULT 4
US-10-223-765-202
; Sequence 202, Application US/10223765
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jin-Soo
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; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park,Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-202

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  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          2 TAGGAGGAT 10


RESULT 5
US-09-882-945A-169/c
; Sequence 169, Application US/09882945A
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-169

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  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
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Db         12 TAGGAGGAT 4


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US-60-216-745-6947
; Sequence 6947, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaure-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY
; FILE REFERENCE: 84.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 6947
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-38923 for SEQ 2416,
US-60-216-745-6947

  Query Match           100.0%;  Score 9;  DB 65;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


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; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaure-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY
; FILE REFERENCE: 84.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 11899
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-43555 for SEQ 2837, in comp
US-60-216-745-11899

  Query Match           100.0%;  Score 9;  DB 65;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          4 TAGGAGGAT 12


RESULT 8
PCT-US00-25479-22/c
; Sequence 22, Application PC/TUS0025479
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590WO
; CURRENT APPLICATION NUMBER: PCT/US00/25479
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 19
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Bisulfite-PCR primer
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: r = G or A
PCT-US00-25479-22

  Query Match             100.0%;  Score 9;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 9
PCT-US00-25479-76
; Sequence 76, Application PC/TUS0025479
; GENERAL INFORMATION:
;  APPLICANT:  The Johns Hopkins University School of Medicine
;  TITLE OF INVENTION:  CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE:  JHU1590WO
;  CURRENT APPLICATION NUMBER: PCT/US00/25479
;  CURRENT FILING DATE:  2000-09-14
;  NUMBER OF SEQ ID NOS:  120
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target sequence for bisulfite-PCR primer
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: y = C or T
PCT-US00-25479-76

  Query Match             100.0%;  Score 9;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


RESULT 10
US-09-398-522-22/c
; Sequence 22, Application US/09398522
; GENERAL INFORMATION:
;  APPLICANT: Issa, Jean-Pierre
;  TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
;  TITLE OF INVENTION: METHODS OF USE THEREFOR
;  FILE REFERENCE: JHU1590
;  CURRENT APPLICATION NUMBER: US/09/398,522
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Bisulfite-PCR primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: r = G or A
US-09-398-522-22

  Query Match             100.0%;  Score 9;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 11
US-09-398-522-76
; Sequence 76, Application US/09398522
; GENERAL INFORMATION:
;  APPLICANT: Issa, Jean-Pierre
;  TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
;  TITLE OF INVENTION: METHODS OF USE THEREFOR
;  FILE REFERENCE: JHU1590
;  CURRENT APPLICATION NUMBER: US/09/398,522
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target sequence for bisulfite-PCR primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: y = C or T
US-09-398-522-76

  Query Match             100.0%;  Score 9;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


RESULT 12
US-60-216-745-8613
; Sequence 8613, Application US/60216745
; GENERAL INFORMATION:
;  APPLICANT:  Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Abderrahim, Hadi
;  APPLICANT:  Dufaure-Gare, Isabelle
;  TITLE OF INVENTION:  BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
;  FILE REFERENCE:  84.US1.PRO
;  CURRENT APPLICATION NUMBER: US/60/216,745
;  CURRENT FILING DATE:  2000-06-30
;  NUMBER OF SEQ ID NOS:  13665
;  SOFTWARE:  Patent.pm
; SEQ ID NO 8613
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-27815 for SEQ 4082,
US-60-216-745-8613

  Query Match             100.0%;  Score 9;  DB 65;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
```

```
              |||||||||
Db          7 TAGGAGGAT 15


RESULT 13
PCT-US01-01857-19
; Sequence 19, Application PC/TUS0101857
; GENERAL INFORMATION:
;  APPLICANT:  Patience, Clive
;  TITLE OF INVENTION:  Swine Defective for Transmission of Porcine Endogenous
;  TITLE OF INVENTION:  Retrovirus and Uses Thereof
;  FILE REFERENCE:  61750-311
;  CURRENT APPLICATION NUMBER: PCT/US01/01857
;  CURRENT FILING DATE:  2001-01-19
;  PRIOR APPLICATION NUMBER:  U.S. 60/243695
;  PRIOR FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  U.S. 60/182965
;  PRIOR FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER:  U.S. 60/177003
;  PRIOR FILING DATE:  2000-01-19
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   OTHER INFORMATION: sequence used in amplification of PERV-sequences.
PCT-US01-01857-19

  Query Match             100.0%;  Score 9;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          2 TAGGAGGAT 10


RESULT 14
PCT-US02-10529-162
; Sequence 162, Application PC/TUS0210529
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTSP-0291
;  CURRENT APPLICATION NUMBER: PCT/US02/10529
;  CURRENT FILING DATE:  2002-04-02
;  PRIOR APPLICATION NUMBER: 09/828,344
;  PRIOR FILING DATE: 2001-04-05
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 162
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-10529-162

  Query Match             100.0%;  Score 9;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 15
PCT-US02-10529-163
; Sequence 163, Application PC/TUS0210529
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTSP-0291
;  CURRENT APPLICATION NUMBER: PCT/US02/10529
;  CURRENT FILING DATE:  2002-04-02
;  PRIOR APPLICATION NUMBER: 09/828,344
;  PRIOR FILING DATE: 2001-04-05
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 163
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-10529-163

  Query Match             100.0%;  Score 9;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          3 TAGGAGGAT 11


Search completed: June  2, 2003, 23:00:11
Job time : 1863.56 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:06:10 ; Search time 176.707 Seconds
(without alignments)
823.475 Million cell updates/sec

Title: US-09-540-843-4
Perfect score: 5
Sequence: 1 gtatg 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		5	100.0	5	6	AX268756	AX268756 Sequence
2	c	5	100.0	5	6	AX268758	AX268758 Sequence
3		5	100.0	7	6	AX268755	AX268755 Sequence
4		5	100.0	7	6	AX268759	AX268759 Sequence
5	c	5	100.0	8	6	AX047565	AX047565 Sequence
6		5	100.0	8	6	AX104946	AX104946 Sequence
7		5	100.0	8	6	AX119567	AX119567 Sequence
8		5	100.0	9	6	AX268753	AX268753 Sequence
9		5	100.0	9	9	S50583	S50583 type I proc
10		5	100.0	9	9	S50585	S50585 type I proc
11		5	100.0	10	6	A18263	A18263 oligonucleo
12	c	5	100.0	10	6	AR065157	AR065157 Sequence
13		5	100.0	10	6	AR079101	AR079101 Sequence
14		5	100.0	10	6	AR079103	AR079103 Sequence
15		5	100.0	10	6	AR098909	AR098909 Sequence
16	c	5	100.0	10	6	AR107335	AR107335 Sequence
17		5	100.0	10	6	AR107344	AR107344 Sequence
18		5	100.0	10	6	AR123039	AR123039 Sequence
19	c	5	100.0	10	6	AR136787	AR136787 Sequence
20		5	100.0	10	6	AR160130	AR160130 Sequence
21		5	100.0	10	6	AR202278	AR202278 Sequence
22		5	100.0	10	6	AX080424	AX080424 Sequence
23		5	100.0	10	6	AX104930	AX104930 Sequence
24		5	100.0	10	6	AX112988	AX112988 Sequence
25	c	5	100.0	10	6	AX112993	AX112993 Sequence
26	c	5	100.0	10	6	AX113002	AX113002 Sequence
27		5	100.0	10	6	AX152720	AX152720 Sequence
28		5	100.0	10	6	AX152760	AX152760 Sequence
29		5	100.0	10	6	AX152761	AX152761 Sequence
30	c	5	100.0	10	6	AX153151	AX153151 Sequence
31		5	100.0	10	6	AX153528	AX153528 Sequence
32	c	5	100.0	10	6	AX153564	AX153564 Sequence
33	c	5	100.0	10	6	AX153578	AX153578 Sequence
34	c	5	100.0	10	6	AX153616	AX153616 Sequence
35		5	100.0	10	6	AX252791	AX252791 Sequence
36		5	100.0	10	6	AX252792	AX252792 Sequence
37	c	5	100.0	10	6	AX252795	AX252795 Sequence
38	c	5	100.0	10	6	AX252796	AX252796 Sequence
39		5	100.0	10	6	AX252827	AX252827 Sequence
40		5	100.0	10	6	AX252828	AX252828 Sequence
41	c	5	100.0	10	6	AX252832	AX252832 Sequence
42		5	100.0	10	6	AX252867	AX252867 Sequence
43		5	100.0	10	6	AX252869	AX252869 Sequence
44	c	5	100.0	10	6	AX252871	AX252871 Sequence
45	c	5	100.0	10	6	AX252873	AX252873 Sequence

ALIGNMENTS

RESULT 1
AX268756
LOCUS AX268756 5 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 4 from Patent WO0174342.
ACCESSION AX268756
VERSION AX268756.1 GI:16541828
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 4 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

```
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        1 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 2
AX268758/c
LOCUS       AX268758                  5 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 6 from Patent WO0174342.
ACCESSION   AX268758
VERSION     AX268758.1  GI:16541830
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 6 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        2 a      2 c      0 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 3
AX268755
LOCUS       AX268755                  7 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 3 from Patent WO0174342.
ACCESSION   AX268755
VERSION     AX268755.1  GI:16541827
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 3 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 4
AX268759
LOCUS       AX268759                  7 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 7 from Patent WO0174342.
ACCESSION   AX268759
VERSION     AX268759.1  GI:16541831
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 7 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      2 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 5
AX047565/c
LOCUS       AX047565                  8 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 6 from Patent WO0068399.
ACCESSION   AX047565
VERSION     AX047565.1  GI:11876656
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Mcivor,R.S., Hackett,P.B. and Aguilar-Cordova,E.
  TITLE     Vector-mediated delivery of integrating transposon sequences
  JOURNAL   Patent: WO 0068399-A 6 16-NOV-2000;
            REGENTS OF THE UNIVERSITY OF MINNESOTA (US) ; BAYLOR COLLEGE OF
            MEDICINE (US) ; McIvor, R. Scott (US) ; Hackett, Perry B. (US) ;
            Aguilar-Cordova, Estuardo (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Direct Repeat Sequence"
BASE COUNT        4 a      3 c      0 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2
```

```
RESULT 6
AX104946
LOCUS       AX104946                  8 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1138 from Patent WO0122972.
ACCESSION   AX104946
VERSION     AX104946.1  GI:13921143
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1138 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        2 a      1 c      2 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 7
AX119567
LOCUS       AX119567                  8 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 224 from Patent WO0129251.
ACCESSION   AX119567
VERSION     AX119567.1  GI:14036486
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Messiaen,L. and Callens,T.
  TITLE     Improved mutation analysis of the nf1 gene
  JOURNAL   Patent: WO 0129251-A 224 26-APR-2001;
            UNIVERSITEIT GENT (BE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      0 c      4 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 8
AX268753
LOCUS       AX268753                  9 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1 from Patent WO0174342.
ACCESSION   AX268753
VERSION     AX268753.1  GI:16541825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 1 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      4 g      2 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 9;
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Qy          1 GTATG 5
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Db          3 GTATG 7


RESULT 9
S50583
LOCUS       S50583                    9 bp    mRNA    linear   PRI 07-MAY-1993
DEFINITION  type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION   S50583
VERSION     S50583.1  GI:233928
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
  TITLE     Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
  JOURNAL   J. Biol. Chem. 266 (24), 15608-15613 (1991)
  MEDLINE   91340689
   PUBMED   1874719
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 50583] from the original journal article.
            This sequence comes from Fig 5A.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .9
                     /gene="type I procollagen"
BASE COUNT        1 a      3 c      2 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 9


RESULT 10
S50585
LOCUS       S50585                    9 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  type I procollagen [human, Genomic Mutant, 9 nt].
ACCESSION   S50585
VERSION     S50585.1  GI:233929
KEYWORDS    .
SOURCE      Homo sapiens.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
  TITLE     Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
  JOURNAL   J. Biol. Chem. 266 (24), 15608-15613 (1991)
  MEDLINE   91340689
   PUBMED   1874719
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 50585] from the original journal article.
            This sequence comes from Fig 5B.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .9
                     /gene="type I procollagen"
BASE COUNT        2 a      1 c      3 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+09;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 9


RESULT 11
A18263
LOCUS       A18263                    10 bp    DNA     linear   PAT 12-APR-1994
DEFINITION  oligonucleotide.
ACCESSION   A18263
VERSION     A18263.1  GI:512254
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Della Valle,F., Callegaro,L. and Negro,A.
  TITLE     Process for the preparation of genetic vectors for the nerve growth
            factor expression in eukaryotic cells
  JOURNAL   Patent: EP 0432510-A 12 19-JUN-1991;
            FIDIA S.p.A
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      1 c      3 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 10


RESULT 12
AR065157/c
LOCUS       AR065157                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5849489.
ACCESSION   AR065157
VERSION     AR065157.1  GI:5995373
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Heller,M.J.
  TITLE     Hybridization of polynucleotides conjugated with chromophores and
            fluorophores to generate donor-to-donor energy transfer system
  JOURNAL   Patent: US 5849489-A 1 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        3 a      2 c      2 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          8 GTATG 4


RESULT 13
AR079101
LOCUS       AR079101                  10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 23 from patent US 5965409.
ACCESSION   AR079101
VERSION     AR079101.1  GI:10005847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Pardee,A.B. and Liang,P.
  TITLE     System for comparing levels or amounts of mRNAs
  JOURNAL   Patent: US 5965409-A 23 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        1 a      1 c      3 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 14
AR079103
LOCUS       AR079103                  10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 25 from patent US 5965409.
ACCESSION   AR079103
VERSION     AR079103.1  GI:10005849
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Pardee,A.B. and Liang,P.
  TITLE     System for comparing levels or amounts of mRNAs
  JOURNAL   Patent: US 5965409-A 25 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        1 a      2 c      3 g      3 t      1 others
ORIGIN

  Query Match             100.0%;  Score 5;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+06;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTATG 5
              |||||
Db          1 GTATG 5
```

RESULT 15
AR098909
LOCUS AR098909 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 45 from patent US 6077685.
ACCESSION AR098909
VERSION AR098909.1 GI:12808675
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 45 20-JUN-2000;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
BASE COUNT 2 a 2 c 3 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTATG 5
              |||||
Db          1 GTATG 5
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Job time : 177.707 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-540-843-4
Perfect score: 5
Sequence: 1 gtatg 5

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Searched: 2185239 seqs, 1125999159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5	100.0	5	20	AAZ10695	Oligonucleotide se
c	2	5	100.0	5	20	AAZ10696	Oligonucleotide se
	3	5	100.0	5	23	AAS14908	Melanogenesis asso
c	4	5	100.0	5	23	AAS14910	Melanogenesis asso
	5	5	100.0	7	20	AAZ10694	Oligonucleotide se
	6	5	100.0	7	23	AAS14907	Melanogenesis asso
	7	5	100.0	7	23	AAS14911	Melanogenesis asso
c	8	5	100.0	8	22	AAD02250	Direct repeat sequ
	9	5	100.0	9	19	AAV22350	A promoter regulat
	10	5	100.0	9	19	AAV22283	GAS complement gen
	11	5	100.0	9	19	AAV15899	Cyclin D transcrip
	12	5	100.0	9	20	AAZ10692	Oligonucleotide se
	13	5	100.0	9	23	AAS14905	Melanogenesis asso
c	14	5	100.0	9	24	ABQ71504	Zinc finger protei
	15	5	100.0	9	24	ABQ71922	Zinc finger protei
	16	5	100.0	9	24	ABQ71958	Zinc finger protei
c	17	5	100.0	10	14	AAQ43164	Donor oligomer wit
	18	5	100.0	10	15	AAQ71104	Merlin exon 14 spl
	19	5	100.0	10	16	AAQ97224	Oligonucleotide Ec
c	20	5	100.0	10	16	AAX32625	Anticancer duplex
	21	5	100.0	10	17	AAT35734	Primer E19 for V.d
c	22	5	100.0	10	18	AAT66073	(dC-dA)n.(dG-dT)n
	23	5	100.0	10	19	AAV50271	Yeast tag for addi
	24	5	100.0	10	19	AAV50250	Yeast tag for addi
c	25	5	100.0	10	19	AAV50184	Yeast tag for addi
c	26	5	100.0	10	19	AAV50127	Yeast tag for NORF
	27	5	100.0	10	19	AAV35934	Primer used in RAP
	28	5	100.0	10	19	AAV35910	Primer used in RAP
	29	5	100.0	10	20	AAX18629	p53 serial analysi
c	30	5	100.0	10	20	AAV73806	Chromophore contai
c	31	5	100.0	10	21	AAC73931	Human dendritic ce
c	32	5	100.0	10	21	AAC74120	Human monocyte and
	33	5	100.0	10	21	AAC74154	Human monocyte and
c	34	5	100.0	10	21	AAA93858	Oligonucleotide us
	35	5	100.0	10	21	AAA93865	Oligonucleotide us
	36	5	100.0	10	21	AAA53110	Mouse DNA adapter
c	37	5	100.0	10	21	AAA15244	Primer MR15 for mo
	38	5	100.0	10	21	AAA56166	Human monocyte gen
	39	5	100.0	10	21	AAA56218	Human macrophage g
c	40	5	100.0	10	21	AAA56224	Human macrophage g
	41	5	100.0	10	21	AAA56294	Human macrophage g
c	42	5	100.0	10	21	AAA56321	Human macrophage g
	43	5	100.0	10	21	AAA56331	Human macrophage g
	44	5	100.0	10	21	AAA56407	Human macrophage g
c	45	5	100.0	10	21	AAA56440	Human macrophage g

ALIGNMENTS

RESULT 1
AAZ10695
ID AAZ10695 standard; DNA; 5 BP.
XX
AC AAZ10695;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 1 GTATG 5

RESULT 2
AAZ10696/c
ID AAZ10696 standard; DNA; 5 BP.
XX
AC AAZ10696;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 5 GTATG 1

RESULT 3
AAS14908
ID AAS14908 standard; DNA; 5 BP.
XX
AC AAS14908;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #4.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #4, a truncated
CC version of the oligonucleotide shown in AAS14906, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

```
  Query Match           100.0%;  Score 5;  DB 23;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 4.3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 4
AAS14910/c
ID   AAS14910 standard; DNA; 5 BP.
XX
AC   AAS14910;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #6.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #6, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell proliferation,
CC   described in the method of the invention.
XX
SQ   Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 23;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 4.3e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 5
AAZ10694
ID   AAZ10694 standard; DNA; 7 BP.
XX
AC   AAZ10694;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW   p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW   UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW   atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW   skin cancer; ss.
XX
OS   Synthetic.
XX
PN   GB2336157-A.
XX
PD   13-OCT-1999.
XX
PF   24-MAR-1999;   99GB-0006758.
XX
PR   26-MAR-1998;   98US-0048927.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 1999-543520/46.
XX
PT   DNA fragments useful for increasing p53 activity in a cell and reducing
PT   susceptibility to UV-induced hyperproliferative diseases -
XX
PS   Claim 11; Page 30; 44pp; English.
XX
CC   AAZ10692-97 represent DNA fragments that are used for increasing p53
CC   activity in a cell. The oligonucleotides are are UV mimetics and
CC   protect cells against subsequent exposure to UV-irradiation or
CC   chemicals. The oligonucleotides are useful for increasing p53 activity
CC   in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC   diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC   rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC   and reducing susceptibility to skin cancer.
XX
SQ   Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 20;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 6
AAS14907
ID   AAS14907 standard; DNA; 7 BP.
XX
AC   AAS14907;
```

```
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #3.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #3, a truncated
CC   version of the oligonucleotide shown in AAS14906, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 23;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 7
AAS14911
```

```
ID   AAS14911 standard; DNA; 7 BP.
XX
AC   AAS14911;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #7.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag= a
FT                    /mod_base= a
FT                    /note= "Phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 38; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #7, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 23;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 GTATG 5
              |||||
Db          2 GTATG 6
```

RESULT 8
AAD02250/c
ID AAD02250 standard; DNA; 8 BP.
XX
AC AAD02250;
XX
DT 28-MAR-2001 (first entry)
XX
DE Direct repeat sequence that binds to SB protein.
XX
KW Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
KW non-integrating viral vector; cytostatic; anti-diabetic; cardiant;
KW neuroprotective; genetic disease; gene therapy; therapy; cancer;
KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;
KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
XX
OS Unidentified.
XX
PN WO200068399-A2.
XX
PD 16-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12827.
XX
PR 11-MAY-1999; 99US-0133569.
XX
PA (MINU) UNIV MINNESOTA.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MCIV/) MCIVOR R S.
PA (HACK/) HACKETT P B.
PA (AGUI/) AGUILAR-CORDOVA E.
XX
PI Mcivor RS, Hackett PB, Aguilar-Cordova E;
XX
DR WPI; 2001-024870/03.
XX
PT Non-integrating (adenovirus-based) viral vectors useful in gene
PT therapy, especially for treating patients suffering from a genetic
PT disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer
PT or brain malfunction -
XX
PS Disclosure; Page 14; 62pp; English.
XX
CC The patent discloses non-integrating viral vectors comprising a
CC polynucleotide flanked by inverted repeats that bind a transposase, a
CC transposase-encoding polynucleotide operably linked to a regulatory
CC sequence comprising an operator, that alters expression of the
CC transposase-encoding polynucleotide. Transposon sequences can integrate
CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB
CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating
CC vector. The non-integrating viral vectors are useful for treating
CC genetic disease characterised by subnormal production of a polypeptide or
CC RNA, e.g. for replacement of a defective gene, delivery of a polypeptide
CC drug or supplementation of a metabolic activity. These genetic diseases
CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or
CC brain malfunction. The non-integrating viral vectors are useful as
CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy
CC and can also be used for applications that involve long-term production
CC of a polypeptide. The non-integrating viral vectors are also useful for
CC creating transgenic host cells that provide normal cells with protection
CC against toxic side effects of chemotherapy.
CC The sequence of the present invention is a direct repeat sequence that
CC binds to SB protein.
XX
SQ Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;

```
  Query Match            100.0%;  Score 5;  DB 22;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2
```

RESULT 9
AAV22350
ID AAV22350 standard; RNA; 9 BP.
XX
AC AAV22350;
XX
DT 29-JUN-1998 (first entry)
XX
DE A promoter regulatory motif found in the utrons of the invention.
XX
KW 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;
KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
KW HIV gene expression; transplant rejection; treatment;
KW autoimmune disease; inflammatory disease; ss.
XX
OS Unidentified.
XX
PN WO9744450-A1.
XX
PD 27-NOV-1997.
XX
PF 21-MAY-1997; 97WO-US09459.
XX
PR 21-MAY-1996; 96US-0646789.
XX
PA (UYYA) UNIV YALE.
XX
PI Peyman JA;
XX
DR WPI; 1998-018505/02.
XX
PT Utrons, RNA molecules containing promoter regulatory motifs -
PT useful to suppress express expression from promoter of interest,
PT specifically TSU nucleic acid suppression of MHC Class I and II gene
PT expression
XX
PS Claim 20; Page 20; 200pp; English.
XX
CC The present sequence represents a promoter regulatory element,
CC found in the utrons of the invention. Utrons are from, or are
CC homologous to, the 3' untranslated region (UTR), of an mRNA that
CC stimulates or inhibits a cellular response by sequence specific
CC interactions. The utron is able to suppress constitutive and
CC interferon-gamma (IFN-gamma) induced major histocompatibility complex
CC (MHC) class I and class II antigen expression and expression of other
CC antigens, the gene promoters of which contain related sequence motifs
CC that are stimulated by the same factors which stimulate MHC class I and
CC class II antigen expression. Such utrons can be used to regulate
CC gene expression in a subject, e.g. a human or a cell in vitro,
CC specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2,
CC Fc gamma R, IL-2 or HIV gene expression. They can be used to inhibit
CC transplant rejection, or treat an autoimmune or inflammatory disease or
CC disorder.
XX
SQ Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;

```
  Query Match            100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 2.4e+08;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |:|:|
Db          1 GUAUG 5
```

```
RESULT 10
AAV22283
ID   AAV22283 standard; DNA; 9 BP.
XX
AC   AAV22283;
XX
DT   29-JUN-1998  (first entry)
XX
DE   GAS complement gene promoter motif found in a trophoblast STAT utron.
XX
KW   Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; class I; class II; IFN signalling;
KW   GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7;
KW   B7-1; B7-2; Fc gamma R; HIV gene expression; transplant rejection;
KW   treatment; autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US09459.
XX
PR   21-MAY-1996;   96US-0646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs  -
PT   useful to suppress express expression from promoter of interest,
PT   specifically TSU nucleic acid suppression of MHC Class I and II gene
PT   expression
XX
PS   Claim 22; Page 90; 200pp; English.
XX
CC   The present sequence represents a GAS complement gene promoter motif
CC   found in a trophoblast STAT utron (TSU). TSUs be isolated from a CDNA
CC   library prepared from mRNA isolated from trophoblast cells. Utrons are
CC   from, or are homologous to, the 3' untranslated region (UTR), of an mRNA
CC   that stimulates or inhibits a cellular response by sequence specific
CC   interactions. The TSU is able to suppress constitutive and
CC   interferon-gamma (IFN-gamma) induced major histocompatibility complex
CC   (MHC) class I and class II antigen expression and expression of other
CC   antigens, the gene promoters of which contain related sequence motifs
CC   that are stimulated by the same factors which stimulate MHC class I and
CC   class II antigen expression. The TSU sequence contains motifs related to
CC   IFN signalling (GAS, ISRE and interleukin-4 response elements). The
CC   nucleic acid can be used to regulate gene expression in a subject, e.g. a
CC   human or a cell in vitro, specifically inhibiting MHC Class I or II,
CC   ICAM-7, B7-1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be
CC   used to inhibit transplant rejection, or treat an autoimmune or
CC   inflammatory disease or disorder. It can also be used to inhibit the
CC   action of STAT1-6, or a cytokine.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 11
AAV15899
ID   AAV15899 standard; DNA; 9 BP.
XX
AC   AAV15899;
XX
DT   26-MAY-1998  (first entry)
XX
DE   Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX
KW   cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW   cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW   nonamer consensus sequence; ss.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
PN   WO9743415-A1.
XX
PD   20-NOV-1997.
XX
PF   16-MAY-1997;   97WO-US08480.
XX
PR   15-MAY-1997;   97US-0017815.
PR   16-MAY-1996;   96US-0017815.
PR   16-MAY-1996;   96US-0648837.
XX
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Hirai H,  Inoue K,  Sherr CJ;
XX
DR   WPI; 1998-008884/01.
XX
PT   Cyclin D transcription factor and related DNA - can be used to
PT   develop products for treatment of, e.g. cancer
XX
PS   Claim 3; Page 99; 120pp; English.
XX
CC   This is a nonamer consensus sequence of a cyclin D transcription factor
CC   DMP1. DMP1 is an amino acid polymer which has binding affinity for a
CC   D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and
CC   is a transcription factor involved in the activation of genes that
CC   prevent cell proliferation. The DMP1 nucleic acid is operatively linked
CC   to an expression control sequence in an expression vector. The expression
CC   vector has a transcription control sequence comprising this nonamer
CC   sequence operably associated with a recombinant gene or a cassette
CC   insertion site for a recombinant gene. The vector is homologously
CC   recombined in a chromosome of a transgenic animal. A probe or a
CC   competitor in DMP1 transactivation assays is designed based on this
CC   nonamer sequence.The presence of activity of DMP1 can be determined by
CC   detecting binding of DMP1 and a probe by contacting a biological sample
CC   from a mammal with the probe under conditions that allow binding of the
CC   probe to DMP1, where the probe  contains the core sequence GTA, and where
CC   the presence or activity of DMP1 is suspected in the sample. DMP1 can
CC   function as a cell cycle inhibitor when expressed in a tumour cell.
CC   Modulating the expression of DMP1 can be used to treat tumours and other
CC   cancers. DMP1 can also be used for controlling expression of heterologous
CC   proteins. Antisense sequences and ribozymes can be used to inhibit
CC   expression of the transcription factor. Detecting the level and activity
CC   of DMP1 in cells is useful for detection of cancer cells or
CC   dysproliferative cells.
XX
SQ   Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;

  Query Match           100.0%;  Score 5;  DB 19;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          4 GTATG 8


RESULT 12
AAZ10692
```

```
ID   AAZ10692 standard; DNA; 9 BP.
XX
AC   AAZ10692;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW   p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW   UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW   atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW   skin cancer; ss.
XX
OS   Synthetic.
XX
PN   GB2336157-A.
XX
PD   13-OCT-1999.
XX
PF   24-MAR-1999;   99GB-0006758.
XX
PR   26-MAR-1998;   98US-0048927.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 1999-543520/46.
XX
PT   DNA fragments useful for increasing p53 activity in a cell and reducing
PT   susceptibility to UV-induced hyperproliferative diseases -
XX
PS   Claim 11; Page 29; 44pp; English.
XX
CC   AAZ10692-97 represent DNA fragments that are used for increasing p53
CC   activity in a cell. The oligonucleotides are are UV mimetics and
CC   protect cells against subsequent exposure to UV-irradiation or
CC   chemicals. The oligonucleotides are useful for increasing p53 activity
CC   in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC   diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC   rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC   and reducing susceptibility to skin cancer.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 20;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 13
AAS14905
ID   AAS14905 standard; DNA; 9 BP.
XX
AC   AAS14905;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #1.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= g
FT                   /note= "Optionally phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light  -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #1, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 5;  DB 23;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 14
ABQ71504/c
ID   ABQ71504 standard; DNA; 9 BP.
XX
AC   ABQ71504;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:623.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
```

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 45; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;

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  Query Match            100.0%;  Score 5;  DB 24;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2
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RESULT 15
ABQ71922
ID ABQ71922 standard; DNA; 9 BP.
XX
AC ABQ71922;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2220.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 58; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;

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  Query Match            100.0%;  Score 5;  DB 24;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          4 GTATG 8
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Search completed: June 2, 2003, 18:45:12
Job time : 84.7366 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:29:55 ; Search time 627.439 Seconds
(without alignments)
129.060 Million cell updates/sec

Title: US-09-540-843-4
Perfect score: 5
Sequence: 1 gtatg 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	5	100.0	14	13	BM398220	BM398220 5009-0-42
c 2	5	100.0	16	9	AI424037	AI424037 tf51h06.x
c 3	5	100.0	16	9	AI685758	AI685758 tu37g09.x
c 4	5	100.0	16	9	AI721735	AI721735 fc31g08.x
c 5	5	100.0	16	13	BG928185	BG928185 HNC65-1-D
c 6	5	100.0	17	13	BG929060	BG929060 HNC11-1-G
c 7	5	100.0	17	14	C21103	C21103 HUMGS000262
c 8	5	100.0	18	13	BM397954	BM397954 5009-0-39
9	5	100.0	19	9	AA977115	AA977115 oq24c08.s
c 10	5	100.0	19	9	AI120725	AI120725 ub72b11.r
11	5	100.0	19	9	AI747751	AI747751 ul21h05.x
12	5	100.0	19	14	C00646	C00646 HUMGS000819
13	5	100.0	19	17	AZ341880	AZ341880 1M0074O04
c 14	5	100.0	19	17	AZ345849	AZ345849 1M0080D16
c 15	5	100.0	19	17	AZ355195	AZ355195 1M0094G22
c 16	5	100.0	19	17	AZ406137	AZ406137 1M0175F16
17	5	100.0	19	17	AZ422163	AZ422163 1M0200B22
18	5	100.0	19	17	AZ434551	AZ434551 1M0221C12
c 19	5	100.0	19	17	AZ464990	AZ464990 1M0274G11
c 20	5	100.0	19	17	AZ486152	AZ486152 1M0314A04
21	5	100.0	19	17	AZ579566	AZ579566 1M0367L08
c 22	5	100.0	19	17	AZ614702	AZ614702 1M0443F10
c 23	5	100.0	19	17	AZ626685	AZ626685 1M0467M01
24	5	100.0	19	17	AZ645469	AZ645469 1M0510L24
25	5	100.0	19	17	AZ647364	AZ647364 1M0513O16
26	5	100.0	19	17	AZ759906	AZ759906 1M0553C10
27	5	100.0	19	17	AZ766086	AZ766086 1M0563G19
c 28	5	100.0	19	17	AZ799396	AZ799396 2M0056N18
c 29	5	100.0	19	17	AZ815067	AZ815067 2M0083P01
30	5	100.0	19	17	AZ817238	AZ817238 2M0086E01
c 31	5	100.0	19	17	AZ839614	AZ839614 2M0135N16
c 32	5	100.0	19	17	AZ864822	AZ864822 2M0174C08
c 33	5	100.0	19	17	AZ942806	AZ942806 2M0203F09
c 34	5	100.0	19	17	AZ948421	AZ948421 2M0211A01
35	5	100.0	19	17	AZ949895	AZ949895 2M0213N08
36	5	100.0	19	17	AZ953217	AZ953217 2M0218A23
c 37	5	100.0	19	17	AZ987324	AZ987324 2M0269B21
c 38	5	100.0	19	17	AZ990856	AZ990856 2M0274F14
c 39	5	100.0	20	17	AZ336039	AZ336039 1M0066E09
c 40	5	100.0	20	17	AZ359199	AZ359199 1M0101M19
c 41	5	100.0	20	17	AZ369273	AZ369273 1M0119H13
42	5	100.0	20	17	AZ387347	AZ387347 1M0146K12
43	5	100.0	20	17	AZ391065	AZ391065 1M0152H20
44	5	100.0	20	17	AZ398474	AZ398474 1M0163G20
c 45	5	100.0	20	17	AZ406839	AZ406839 1M0176C16

ALIGNMENTS

RESULT 1
BM398220/c
LOCUS BM398220 14 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398220
VERSION BM398220.1 GI:18198273
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 14)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel ,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .14
/organism="Tetrahymena thermophila"
/strain="CU428.1"

/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 4 a 5 c 0 g 5 t
ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 5 GTATG 1

RESULT 2
AI424037/c
LOCUS AI424037 16 bp mRNA linear EST 09-MAR-1999
DEFINITION tf51h06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2102843 3' similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION AI424037
VERSION AI424037.1 GI:4269968
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .16
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 8 a 6 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 6 GTATG 2

RESULT 3
AI685758/c
LOCUS AI685758 16 bp mRNA linear EST 27-MAY-1999
DEFINITION tu37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253280 3' similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL SEQUENCE MOTIF PROTEIN 1 ;contains element LTR4 repetitive element ;, mRNA sequence.
ACCESSION AI685758
VERSION AI685758.1 GI:4897052
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .16
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2253280"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 7 a 7 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 9 GTATG 5

RESULT 4
AI721735/c
LOCUS AI721735 16 bp mRNA linear EST 07-JUN-2001
DEFINITION fc31g08.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone

```
            IMAGE:3723038 3' similar to SW:YM14_PARTE P15615 HYPOTHETICAL 47.2
            KD PROTEIN ;, mRNA sequence.
ACCESSION   AI721735
VERSION     AI721735.1  GI:5040064
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fc31g08.y1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:3723038"
                     /clone_lib="Zebrafish WashU MPIMG EST"
                     /sex="mixed"
                     /tissue_type="26 somite embryos, adult livers, shield
                     stage embryos"
                     /lab_host="XL1-blue MRF"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'];
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
                     Institut fuer Molekulare Genetik,Berlin). cDNAs for EST
                     analysis were selected following oligonucleotide
                     hybridization fingerprinting of arrayed clones from
                     zebrafish late somitogenesis (26 ss), adult liver or
                     embryonic shield stage (5.6 h) libraries.  Fingerprint
                     data were used to computationally cluster cDNAs, and a
                     single cDNA from each cluster was chosen for sequencing.
                     In some cases multiple members of the same cluster were
                     sequenced to assess clustering parameters or single clones
                     were sequenced additional times to assess quality
                     control."
BASE COUNT        6 a      8 c      1 g      1 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db         13 GTATG 9


RESULT 5
BG928185/c
LOCUS       BG928185                 16 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA,
            mRNA sequence.
ACCESSION   BG928185
VERSION     BG928185.1  GI:14322708
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"
BASE COUNT        4 a      6 c      2 g      3 t      1 others
ORIGIN

  Query Match             100.0%;  Score 5;  DB 13;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db         12 GTATG 8


RESULT 6
BG929060/c
LOCUS       BG929060                 17 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG929060
VERSION     BG929060.1  GI:14323583
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
```

osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HNC (Human Normal Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"
BASE COUNT 5 a 8 c 2 g 2 t
ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 10 GTATG 6

RESULT 7
C21103/c
LOCUS C21103 17 bp mRNA linear EST 23-OCT-1996
DEFINITION HUMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA sequence.
ACCESSION C21103
VERSION C21103.1 GI:1622213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Okubo,K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
/note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI; Monocytes were prepared from blood by ficoll-hypaque, percoll and T cell rosetting purification steps (purity: 96 %). mRNA was prepared from activated monocytes from a patient with rheumatoid arthritis. mRNA was reverse transcribed with MuLV. Using Eco-RI linkers cDNA was cloned into l-gt-11 vector arms. The cDNA library was screened by differential hybidization using radioactively marked ss-cDNA from activated and non-activated monocytes. "
BASE COUNT 5 a 5 c 2 g 5 t
ORIGIN

Query Match 100.0%; Score 5; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 13 GTATG 9

RESULT 8
BM397954/c
LOCUS BM397954 18 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-39-G08.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397954
VERSION BM397954.1 GI:18198022
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 18)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .18
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 3 a 7 c 5 g 3 t
ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 5 GTATG 1

RESULT 9
AA977115
LOCUS AA977115 19 bp mRNA linear EST 26-MAY-1998
DEFINITION oq24c08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587278 3' similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION AA977115
VERSION AA977115.1 GI:3154561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1587278"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        2 a      0 c      7 g     10 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 10
AI120725/c
LOCUS       AI120725                 19 bp    mRNA    linear   EST 02-SEP-1998
DEFINITION  ub72b11.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ;,
            mRNA sequence.
ACCESSION   AI120725
VERSION     AI120725.1  GI:3521049
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:905729
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1383261"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        9 a      3 c      4 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db         11 GTATG 7


RESULT 11
AI747751
LOCUS       AI747751                 19 bp    mRNA    linear   EST 22-JUN-1999
DEFINITION  ul21h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND
            POLYADENYLATION SPECIFITY FACTOR PROTEIN. ;, mRNA sequence.
ACCESSION   AI747751
VERSION     AI747751.1  GI:5126015
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:995933
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: custom primer used
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
```

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     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2088249"
                     /clone_lib="Sugano mouse embryo mewa"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert. Size selection was performed to exclude fragments
                     <1.5kb. Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT        6 a      2 c      8 g      3 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db         13 GTATG 17


RESULT 12
C00646
LOCUS       C00646                  19 bp    mRNA    linear   EST 23-JUL-1996
DEFINITION  HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C00646
VERSION     C00646.1  GI:1432876
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            Human Gene Signature, 3'-directed cDNA sequence. We are not
            submitting the same cDNA sequence redundantly to DDBJ since 1993.
            For the abundance information of clones with this sequence in this
            library and as well as in other 3'-directed libraries, see '
            http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
            represented by this GS sequences is also found there.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human adult (K.Okubo)"
                     /dev_stage="adult"
                     /note="Organ: blood; Vector: l-gt-11; Site_1: Eco-RI;
                     Monocytes were prepared from blood by ficoll-hypaque,
                     percoll and T cell rosetting purification steps (purity:
                     96 %). mRNA was prepared from activated monocytes from a
                     patient with rheumatoid arthritis. mRNA was reverse
                     transcribed with MuLV. Using Eco-RI linkers cDNA was
                     cloned into l-gt-11 vector arms. The cDNA library was
                     screened by differential hybidization using radioactively
                     marked ss-cDNA from activated and non-activated
                     monocytes. "
BASE COUNT        4 a      1 c      8 g      6 t
ORIGIN

  Query Match             100.0%;  Score 5;  DB 14;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db         14 GTATG 18


RESULT 13
AZ341880
LOCUS       AZ341880                19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0074O04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0074O04 R, DNA sequence.
ACCESSION   AZ341880
VERSION     AZ341880.1  GI:10418570
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0074  row: O  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0074O04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
```

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 4 a 4 c 6 g 5 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 8 GTATG 12

RESULT 14
AZ345849/c
LOCUS AZ345849 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080D16 R, DNA sequence.
ACCESSION AZ345849
VERSION AZ345849.1 GI:10425086
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080D16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 9 a 4 c 0 g 6 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 13 GTATG 9

RESULT 15
AZ355195/c
LOCUS AZ355195 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0094G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0094G22 R, DNA sequence.
ACCESSION AZ355195
VERSION AZ355195.1 GI:10467355
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: G column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0094G22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTATG 5
              |||||
Db         12 GTATG 8
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Search completed: June 2, 2003, 20:35:43
Job time : 630.439 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:31:20 ; Search time 20.4878 Seconds
(without alignments)
74.844 Million cell updates/sec

Title: US-09-540-843-4
Perfect score: 5
Sequence: 1 gtatg 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5	100.0	5	3	US-08-855-372B-20	Sequence 20, Appl
	2	5	100.0	5	3	US-09-048-927-4	Sequence 4, Appli
	3	5	100.0	5	4	US-09-498-851-20	Sequence 20, Appl
c	4	5	100.0	7	1	US-08-615-170-10	Sequence 10, Appl
c	5	5	100.0	7	1	US-08-615-170-12	Sequence 12, Appl
	6	5	100.0	7	3	US-09-048-927-3	Sequence 3, Appli
	7	5	100.0	9	2	US-08-583-276-1	Sequence 1, Appli
	8	5	100.0	9	3	US-08-646-789A-8	Sequence 8, Appli
	9	5	100.0	9	3	US-08-646-789A-80	Sequence 80, Appl
	10	5	100.0	9	3	US-09-048-927-1	Sequence 1, Appli
c	11	5	100.0	9	4	US-09-319-648-68	Sequence 68, Appl
	12	5	100.0	10	1	US-08-335-565A-27	Sequence 27, Appl
c	13	5	100.0	10	1	US-08-250-951-1	Sequence 1, Appli
c	14	5	100.0	10	1	US-08-232-233-1	Sequence 1, Appli
c	15	5	100.0	10	1	US-08-222-177A-422	Sequence 422, App
	16	5	100.0	10	1	US-08-351-748-23	Sequence 23, Appl
	17	5	100.0	10	1	US-08-351-748-25	Sequence 25, Appl
c	18	5	100.0	10	1	US-08-202-927-25	Sequence 25, Appl
	19	5	100.0	10	1	US-08-430-536A-23	Sequence 23, Appl
	20	5	100.0	10	1	US-08-430-536A-25	Sequence 25, Appl
	21	5	100.0	10	1	US-08-171-718-45	Sequence 45, Appl
c	22	5	100.0	10	2	US-08-703-601-1	Sequence 1, Appli
	23	5	100.0	10	2	US-08-684-547-23	Sequence 23, Appl
	24	5	100.0	10	2	US-08-684-547-25	Sequence 25, Appl
	25	5	100.0	10	3	US-08-469-318-174	Sequence 174, App
	26	5	100.0	10	3	US-08-468-609A-174	Sequence 174, App
	27	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
c	28	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
	29	5	100.0	10	3	US-09-063-450-33	Sequence 33, Appl
c	30	5	100.0	10	4	US-09-123-638-1	Sequence 1, Appli
	31	5	100.0	10	4	US-08-646-695-30	Sequence 30, Appl
	32	5	100.0	10	4	US-08-875-533-31	Sequence 31, Appl
	33	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
c	34	5	100.0	10	4	US-09-724-753-1	Sequence 1, Appli
	35	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
c	36	5	100.0	10	5	PCT-US92-09827-1	Sequence 1, Appli
	37	5	100.0	10	5	PCT-US95-01185-174	Sequence 174, App
c	38	5	100.0	10	5	PCT-US95-02419-25	Sequence 25, Appl
	39	5	100.0	10	5	PCT-US96-06053-30	Sequence 30, Appl
c	40	5	100.0	10	6	5198343-3	Patent No. 5198343
	41	5	100.0	11	1	US-08-401-512-19	Sequence 19, Appl
	42	5	100.0	11	1	US-08-147-696E-4	Sequence 4, Appli
	43	5	100.0	11	1	US-08-696-139-6	Sequence 6, Appli
	44	5	100.0	11	1	US-08-484-334-4	Sequence 4, Appli
c	45	5	100.0	11	2	US-08-441-887A-82	Sequence 82, Appl

ALIGNMENTS

```
RESULT 1
US-08-855-372B-20
; Sequence 20, Application US/08855372B
; Patent No. 6090549
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking Hybridization as a Di
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,372B
;      FILING DATE:  13-MAY-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6090549 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-08-855-372B-20

  Query Match             100.0%;  Score 5;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 2
US-09-048-927-4
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-4

  Query Match             100.0%;  Score 5;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 3
US-09-498-851-20
; Sequence 20, Application US/09498851
; Patent No. 6440671
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous
;    TITLE OF INVENTION:  Stacking Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/498,851
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,372
;      FILING DATE:  13-MAY-97
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6440671 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-09-498-851-20

  Query Match             100.0%;  Score 5;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 4
US-08-615-170-10/c
; Sequence 10, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  10:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..7
;      OTHER INFORMATION:  /standard_name= "Sph-II binding
;      OTHER INFORMATION:  site in SV40"
US-08-615-170-10

  Query Match             100.0%;  Score 5;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 5
US-08-615-170-12/c
; Sequence 12, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..7
;      OTHER INFORMATION:  /standard_name= "Rat beta-Myosin
;      OTHER INFORMATION:  Heavy Chain M-CAT binding element"
US-08-615-170-12

  Query Match             100.0%;  Score 5;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 6
US-09-048-927-3
; Sequence 3, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-3

  Query Match             100.0%;  Score 5;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 7
US-08-583-276-1
; Sequence 1, Application US/08583276
; Patent No. 5837536
;  GENERAL INFORMATION:
;    APPLICANT:  McDonagh, Kevin T.
;    APPLICANT:  Nienhuis, Arthur
;    APPLICANT:  Tolstoshev, Paul
;    TITLE OF INVENTION:  IMPROVED EXPRESSION OF HUMAN
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE GENES AND IMPROVED
;    TITLE OF INVENTION:  SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/583,276
;      FILING DATE:  05-JAN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/332,444
;      FILING DATE:  31-OCT-1994
;      APPLICATION NUMBER:  07/887,712
;      FILING DATE:  22-MAY-1992
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
US-08-583-276-1

  Query Match             100.0%;  Score 5;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          4 GTATG 8


RESULT 8
US-08-646-789A-8
; Sequence 8, Application US/08646789A
; Patent No. 6022863
;  GENERAL INFORMATION:
;    APPLICANT:  Peyman, John A.
;    TITLE OF INVENTION:  REGULATION OF GENE EXPRESSION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,789A
;      FILING DATE:  May 21, 1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6523-006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-646-789A-8

  Query Match             100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 9
US-08-646-789A-80
; Sequence 80, Application US/08646789A
; Patent No. 6022863
;  GENERAL INFORMATION:
;    APPLICANT:  Peyman, John A.
;    TITLE OF INVENTION:  REGULATION OF GENE EXPRESSION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,789A
;      FILING DATE:  May 21, 1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  6523-006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-646-789A-80

  Query Match             100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+07;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |:|:|
Db          1 GUAUG 5


RESULT 10
US-09-048-927-1
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT: Yaar, Mina
;  APPLICANT: Eller, Mark
;  TITLE OF INVENTION: Use of Locally Applied DNA Fragments
;  FILE REFERENCE: BU94-68A2
;  CURRENT APPLICATION NUMBER: US/09/048,927
;  CURRENT FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/952,697
;  EARLIER FILING DATE: 1996-06-03
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;  EARLIER APPLICATION NUMBER: 08/467,012
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-1

  Query Match             100.0%;  Score 5;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          3 GTATG 7


RESULT 11
US-09-319-648-68/c
; Sequence 68, Application US/09319648
; Patent No. 6451530
;   GENERAL INFORMATION:
;        APPLICANT: Hawkins, Mary
;        TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
;                            Formation for Detection of Nucleic Acid Hybridization
;        NUMBER OF SEQUENCES: 68
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/319,648
;             FILING DATE: 30-Jul-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/032,844
;             FILING DATE: 13-DEC-1996
;             APPLICATION NUMBER: WO PCT/US97/22448
;             FILING DATE: 10-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fang, Carol
;             REGISTRATION NUMBER: 48,631
;             REFERENCE/DOCKET NUMBER: 015280-288100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 68:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

  Query Match             100.0%;  Score 5;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          7 GTATG 3


RESULT 12
US-08-335-565A-27
; Sequence 27, Application US/08335565A
; Patent No. 5527671
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Kening
;    APPLICANT:  Rouse, Douglas I.
;    APPLICANT:  German, Thomas L.
;    TITLE OF INVENTION:  ASSAY FOR VERTICILLIUM DAHLIAE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles and Brady
;      STREET:  1 South Pinckney St., PO BOX 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,565A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  960296.93065
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-335-565A-27

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 10


RESULT 13
US-08-250-951-1/c
; Sequence 1, Application US/08250951
; Patent No. 5532129
;  GENERAL INFORMATION:
;    APPLICANT:  Heller, Michael J
;    TITLE OF INVENTION:  SELF-ORGANIZING MOLECULAR PHOTONIC
;    TITLE OF INVENTION:  STRUCTURES BASED ON CHROMOPHORE- AND FLUROPHORE-CONTAINING
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND METHODS OF THEIR USE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bingham & Fitting
;      STREET:  12526 High Bluff Drive, Suite 300
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92130
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/250,951
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/790,262
;       FILING DATE:  07-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fitting, Thomas
;       REGISTRATION NUMBER:  34,163
;       REFERENCE/DOCKET NUMBER:  HEL0002P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-792-3680
;       TELEFAX:  619-792-8477
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  10
;       OTHER INFORMATION:  /note= "Donor chromophore at the 3'
;       OTHER INFORMATION:  T nucleotide"
US-08-250-951-1

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          8 GTATG 4


RESULT 14
US-08-232-233-1/c
; Sequence 1, Application US/08232233
; Patent No. 5565322
;  GENERAL INFORMATION:
;    APPLICANT:  Michael J. Heller
;    TITLE OF INVENTION:  SELF-ORGANIZING MOLECULAR PHOTONIC
;    TITLE OF INVENTION:  STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
;    TITLE OF INVENTION:  CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,233
;      FILING DATE:  May 4, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/790,262
;      FILING DATE:  No. 5565322ember 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, David B.
;      REGISTRATION NUMBER:  31,125
;      REFERENCE/DOCKET NUMBER:  207/170
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  10
;      OTHER INFORMATION:  /note-"Donor chromphore at the 3' T nucleotide"
US-08-232-233-1

  Query Match             100.0%;  Score 5;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          8 GTATG 4


RESULT 15
US-08-222-177A-422/c
; Sequence 422, Application US/08222177A
; Patent No. 5582979
;  GENERAL INFORMATION:
;    APPLICANT:  Weber, James L.
;    TITLE OF INVENTION:  LENGTH POLYMORPHISMS IN
;    TITLE OF INVENTION:  (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  460
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DeWitt Ross & Stevens, S.C.
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/222,177A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/341,562
;      FILING DATE:  21-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sara, Charles S.
;      REGISTRATION NUMBER:  30,492
;      REFERENCE/DOCKET NUMBER:  09865.601
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  422:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-422

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5
|||||
Db 8 GTATG 4

Search completed: June 2, 2003, 20:38:34
Job time : 21.4878 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 19:09:45 ; Search time 35.4878 Seconds
(without alignments)
189.976 Million cell updates/sec

Title: US-09-540-843-4
Perfect score: 5
Sequence: 1 gtatg 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 477662

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5	100.0	5	9	US-10-122-630-4	Sequence 4, Appli
c	2	5	100.0	5	9	US-10-122-630-6	Sequence 6, Appli
	3	5	100.0	5	9	US-10-122-633-4	Sequence 4, Appli
c	4	5	100.0	5	9	US-10-122-633-6	Sequence 6, Appli
	5	5	100.0	7	9	US-10-122-630-3	Sequence 3, Appli
	6	5	100.0	7	9	US-10-122-630-7	Sequence 7, Appli
	7	5	100.0	7	9	US-10-122-633-3	Sequence 3, Appli
	8	5	100.0	7	9	US-10-122-633-7	Sequence 7, Appli
c	9	5	100.0	8	10	US-09-142-593-11	Sequence 11, Appl
c	10	5	100.0	8	10	US-09-927-886-17	Sequence 17, Appl
c	11	5	100.0	8	10	US-09-861-014-6	Sequence 6, Appli
	12	5	100.0	9	9	US-10-122-630-1	Sequence 1, Appli
	13	5	100.0	9	9	US-10-122-633-1	Sequence 1, Appli
c	14	5	100.0	9	9	US-10-096-596-32	Sequence 32, Appl
c	15	5	100.0	9	9	US-09-990-186-623	Sequence 623, App
	16	5	100.0	9	9	US-09-990-186-2220	Sequence 2220, Ap
	17	5	100.0	9	9	US-09-990-186-2256	Sequence 2256, Ap
c	18	5	100.0	9	10	US-09-989-789-623	Sequence 623, App
	19	5	100.0	9	10	US-09-989-789-2220	Sequence 2220, Ap
	20	5	100.0	9	10	US-09-989-789-2256	Sequence 2256, Ap
	21	5	100.0	10	9	US-10-006-542B-5	Sequence 5, Appli
c	22	5	100.0	10	9	US-09-962-602-7	Sequence 7, Appli
	23	5	100.0	10	9	US-09-962-602-8	Sequence 8, Appli
c	24	5	100.0	10	9	US-09-990-186-622	Sequence 622, App
	25	5	100.0	10	9	US-09-990-186-636	Sequence 636, App
	26	5	100.0	10	9	US-09-990-186-1338	Sequence 1338, Ap
	27	5	100.0	10	9	US-09-990-186-1341	Sequence 1341, Ap
	28	5	100.0	10	9	US-09-990-186-1342	Sequence 1342, Ap
	29	5	100.0	10	9	US-09-990-186-1343	Sequence 1343, Ap
c	30	5	100.0	10	10	US-09-822-250-16	Sequence 16, Appl
	31	5	100.0	10	10	US-09-398-399-31	Sequence 31, Appl
c	32	5	100.0	10	10	US-09-989-789-622	Sequence 622, App
	33	5	100.0	10	10	US-09-989-789-636	Sequence 636, App
	34	5	100.0	10	10	US-09-989-789-1338	Sequence 1338, Ap
	35	5	100.0	10	10	US-09-989-789-1341	Sequence 1341, Ap
	36	5	100.0	10	10	US-09-989-789-1342	Sequence 1342, Ap
	37	5	100.0	10	10	US-09-989-789-1343	Sequence 1343, Ap
	38	5	100.0	10	10	US-09-899-381-31	Sequence 31, Appl
c	39	5	100.0	10	12	US-10-033-145-2	Sequence 2, Appli
	40	5	100.0	10	12	US-10-033-145-313	Sequence 313, App
c	41	5	100.0	10	12	US-10-033-145-549	Sequence 549, App
c	42	5	100.0	10	12	US-10-033-145-723	Sequence 723, App
	43	5	100.0	10	12	US-10-033-145-766	Sequence 766, App
	44	5	100.0	10	12	US-10-033-145-824	Sequence 824, App
c	45	5	100.0	10	12	US-10-033-145-979	Sequence 979, App

ALIGNMENTS

RESULT 1
US-10-122-630-4
; Sequence 4, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

Query Match 100.0%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTATG 5
              |||||
Db          1 GTATG 5
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RESULT 2
US-10-122-630-6/c
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

  Query Match            100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 3
US-10-122-633-4
; Sequence 4, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

  Query Match            100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          1 GTATG 5


RESULT 4
US-10-122-633-6/c
; Sequence 6, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

  Query Match            100.0%;  Score 5;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          5 GTATG 1


RESULT 5
US-10-122-630-3
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3
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  Query Match             100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 6
US-10-122-630-7
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

  Query Match             100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 7
US-10-122-633-3
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

  Query Match             100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 8
US-10-122-633-7
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

  Query Match             100.0%;  Score 5;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          2 GTATG 6


RESULT 9
US-09-142-593-11/c
; Sequence 11, Application US/09142593
; Patent No. US20020016975A1
;  GENERAL INFORMATION:
;    APPLICANT:  HACKETT ET AL.
;    TITLE OF INVENTION:  DNA-BASED TRANSPOSON SYSTEM FOR THE
;    TITLE OF INVENTION:  INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MUETING, RAASCH & GEBHARDT, P.A.
;      STREET:  119 NORTH FOURTH STREET, SUITE 203
;      CITY:  MINNEAPOLIS
;      STATE:  MINNESOTA
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/09/142,593
;       FILING DATE:  10-SEP-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/040,664
;       FILING DATE:  11-MAR-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/053,868
;       FILING DATE:  28-JUL-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/065,303
;       FILING DATE:  13-NOV-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US98/04687
;       FILING DATE:  11-MAR-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SANDBERG, VICTORIA A.
;       REGISTRATION NUMBER:  41,287
;       REFERENCE/DOCKET NUMBER:  110.00450101
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612-305-1226
;       TELEFAX:  612-305-1228
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-142-593-11

  Query Match             100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2


RESULT 10
US-09-927-886-17/c
; Sequence 17, Application US/09927886
; Patent No. US20020103152A1
; GENERAL INFORMATION:
;  APPLICANT: Kay, Mark A.
;  APPLICANT:  Yant, Stephen
;  TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
;  TITLE OF INVENTION:  Sleeping Beauty Transposon System
;  FILE REFERENCE: STAN-160CIP
;  CURRENT APPLICATION NUMBER: US/09/927,886
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: 60/162,279
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 09/440,301
;  PRIOR FILING DATE: 1999-11-17
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: transposon repeat sequence
US-09-927-886-17

  Query Match             100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2


RESULT 11
US-09-861-014-6/c
; Sequence 6, Application US/09861014
; Patent No. US20020115216A1
; GENERAL INFORMATION:
;  APPLICANT: Steer, Clifford
;  APPLICANT:  Kren, Betsy
;  APPLICANT:  Linehan-Stieers, Cheryle
;  APPLICANT:  McIvor, R.
;  APPLICANT:  Hackett, Perry
;  TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
;  FILE REFERENCE: 110.01330101
;  CURRENT APPLICATION NUMBER: US/09/861,014
;  CURRENT FILING DATE:  2001-05-19
;  PRIOR APPLICATION NUMBER: US 60/206,002
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/285,121
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6

  Query Match             100.0%;  Score 5;  DB 10;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+08;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATG 5
              |||||
Db          6 GTATG 2


RESULT 12
US-10-122-630-1
; Sequence 1, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

  Query Match             100.0%;  Score 5;  DB 9;  Length 9;
```

Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTATG 5
              |||||
Db          3 GTATG 7
```

RESULT 13
US-10-122-633-1
; Sequence 1, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTATG 5
              |||||
Db          3 GTATG 7
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RESULT 14
US-10-096-596-32/c
; Sequence 32, Application US/10096596
; Publication No. US20030049653A1
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; APPLICANT: Velculescu, Victor
; APPLICANT: Zhang, Lin
; TITLE OF INVENTION: METHOD FOR SERIAL ANLAYSIS OF GENE EXPRESSION
; FILE REFERENCE: 001107.00242
; CURRENT APPLICATION NUMBER: US/10/096,596
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 08/527,154
; PRIOR FILING DATE: 1995-09-12
; PRIOR APPLICATION NUMBER: US 08/544,861
; PRIOR FILING DATE: 1995-10-18
; PRIOR APPLICATION NUMBER: US 09/107,228
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-596-32

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTATG 5
              |||||
Db          7 GTATG 3
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RESULT 15
US-09-990-186-623/c
; Sequence 623, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 623
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-623

Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTATG 5
              |||||
Db          6 GTATG 2
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:06:10 ; Search time 318.073 Seconds
(without alignments)
823.475 Million cell updates/sec

Title: US-09-540-843-2
Perfect score: 9
Sequence: 1 taggaggat 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		9	100.0	9	6	AX268754	AX268754 Sequence
2	c	9	100.0	16	6	AX419832	AX419832 Sequence
3		9	100.0	20	6	A39511	A39511 Sequence 6
4		9	100.0	20	6	AR166936	AR166936 Sequence
5	c	9	100.0	20	6	AX298850	AX298850 Sequence
6	c	9	100.0	20	6	AX327004	AX327004 Sequence
7	c	9	100.0	20	12	AB069488	AB069488 Synthetic
8	c	9	100.0	22	6	E55148	E55148 Method for
9		9	100.0	23	6	E36547	E36547 Method of g
10		9	100.0	23	6	E40169	E40169 Genetic dia
11	c	9	100.0	23	11	DOGC00506A	L77541 Canis famil
12	c	9	100.0	24	6	AR135197	AR135197 Sequence
13	c	9	100.0	24	6	AR146693	AR146693 Sequence
14	c	9	100.0	24	6	AR152264	AR152264 Sequence
15	c	9	100.0	24	6	AR157802	AR157802 Sequence
16		9	100.0	26	6	AX477111	AX477111 Sequence
17	c	9	100.0	27	6	A94623	A94623 Sequence 6
18	c	9	100.0	27	6	AX017661	AX017661 Sequence
19		9	100.0	28	6	AR143009	AR143009 Sequence
20	c	9	100.0	29	6	I55932	I55932 Sequence 20
21	c	9	100.0	30	6	AX286793	AX286793 Sequence
22	c	9	100.0	36	6	AX044051	AX044051 Sequence
23	c	9	100.0	36	6	AX044105	AX044105 Sequence
24	c	9	100.0	36	6	AX044153	AX044153 Sequence
25		9	100.0	37	6	A08117	A08117 pTG2416 DNA
26	c	9	100.0	39	6	E36735	E36735 Novel DNA p
27	c	9	100.0	40	6	AX147669	AX147669 Sequence
28		8	88.9	12	6	AR105116	AR105116 Sequence
29	c	8	88.9	15	6	AR033402	AR033402 Sequence
30	c	8	88.9	15	6	AR033403	AR033403 Sequence
31		8	88.9	15	6	AR108949	AR108949 Sequence
32	c	8	88.9	15	6	AR113224	AR113224 Sequence
33	c	8	88.9	15	6	AR113225	AR113225 Sequence
34	c	8	88.9	15	6	BD005791	BD005791 Novel pro
35	c	8	88.9	15	6	I57631	I57631 Sequence 16
36	c	8	88.9	15	6	I57632	I57632 Sequence 16
37		8	88.9	16	6	A03756	A03756 Nucleotide
38		8	88.9	16	6	A15048	A15048 Nucleotide
39	c	8	88.9	16	6	A22501	A22501 Oligonucleo
40		8	88.9	16	6	A30883	A30883 Synthetic h
41		8	88.9	16	6	A89421	A89421 Sequence 15
42		8	88.9	16	6	AR035160	AR035160 Sequence
43	c	8	88.9	16	6	AX419833	AX419833 Sequence
44	c	8	88.9	16	6	AX419834	AX419834 Sequence
45	c	8	88.9	16	6	AX419835	AX419835 Sequence

ALIGNMENTS

RESULT 1
AX268754
LOCUS AX268754 9 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 2 from Patent WO0174342.
ACCESSION AX268754
VERSION AX268754.1 GI:16541826
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 2 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

```
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        3 a      0 c      4 g      2 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+09;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          1 TAGGAGGAT 9


RESULT 2
AX419832/c
LOCUS       AX419832                 16 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 169 from Patent WO0198537.
ACCESSION   AX419832
VERSION     AX419832.1  GI:21524199
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
  TITLE     Nucleic acid accessible hybridization sites
  JOURNAL   Patent: WO 0198537-A 169 27-DEC-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      7 c      0 g      4 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         12 TAGGAGGAT 4


RESULT 3
A39511
LOCUS       A39511                   20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 6 from Patent EP0614980.
ACCESSION   A39511
VERSION     A39511.1  GI:2295829
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mehtali,M. and Sorg,T.
  TITLE     TAT transdominant variants from human Immunodeficiency virus
  JOURNAL   Patent: EP 0614980-A 6 14-SEP-1994;
            TRANSGENE SA (FR)
COMMENT     Other publication CA 2112652 940705
            Other publication JP 6234791 940823
            Other publication AU 5280393 940714
            Other publication AU 668441 960502
            Other publication FR 2700169 940708.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a      4 c      7 g      3 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          5 TAGGAGGAT 13


RESULT 4
AR166936
LOCUS       AR166936                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6284252.
ACCESSION   AR166936
VERSION     AR166936.1  GI:16243331
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mehtali,M. and Sorg,T.
  TITLE     Transdominant TAT variants of the human immunodeficiency virus
  JOURNAL   Patent: US 6284252-A 6 04-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      4 c      7 g      3 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db          5 TAGGAGGAT 13


RESULT 5
AX298850/c
LOCUS       AX298850                 20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 484 from Patent WO0183749.
ACCESSION   AX298850
VERSION     AX298850.1  GI:17128840
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 484 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus sp."
                     /db_xref="taxon:10095"
BASE COUNT        3 a      7 c      4 g      6 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9
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RESULT 6
AX327004/c
LOCUS       AX327004                  20 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 200 from Patent WO0178894.
ACCESSION   AX327004
VERSION     AX327004.1  GI:18097715
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Keith,T.
  TITLE     Novel human gene relating to respiratory diseases, obesity, and
            inflammatory bowel disease
  JOURNAL   Patent: WO 0178894-A 200 25-OCT-2001;
            Genome Therapeutics Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        2 a      8 c      4 g      6 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         19 TAGGAGGAT 11


RESULT 7
AB069488/c
LOCUS       AB069488                  20 bp    DNA     linear   SYN 08-AUG-2001
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-W47099 at
            1p36.
ACCESSION   AB069488
VERSION     AB069488.1  GI:15130292
KEYWORDS    .
SOURCE      synthetic construct DNA.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="forward primer for human STS sts-W47099 at 1p36
                     sts-W47099 obtained from clones B61B17, B86A23, B268I12,
                     B316H11, B26P17, B179J2, B166E12, Human BAC library
                     RPCI-11"
BASE COUNT        3 a      9 c      2 g      6 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         20 TAGGAGGAT 12


RESULT 8
E55148/c
LOCUS       E55148                    22 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for determining the presence of apoptosis regulatory
            function of drug Method for determining the presence of apoptosis
            regulatory  function of drug.
ACCESSION   E55148
VERSION     E55148.1  GI:18629759
KEYWORDS    JP 2000217598-A/6.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kamata,S., Tsujimoto,Y., Otsubo,T. and Murakami,Y.
  TITLE     Method for determining the presence of apoptosis regulatory
            function of drug
  JOURNAL   Patent: JP 2000217598-A 6 08-AUG-2000;
            SUMITOMO CHEM CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000217598-A/6
            PD   08-AUG-2000
            PF   29-JAN-1999 JP 1999022356
            PR
            PI   SHINJI KAMATA,YOSHIHIDE TSUJIMOTO,TSUGUTERU OTSUBO, PI   YUKO
            MURAKAMI
            PC   C12Q1/37,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K38/00, PC
              A61K45/00,
            PC   A61K48/00,C12N15/09,G01N33/15,G01N33/50,G01N33/50, PC
            G01N33/68//C07K14/47,
            PC   A61K37/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      6 c      4 g      7 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         14 TAGGAGGAT 6


RESULT 9
E36547
LOCUS       E36547                    23 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method of gene diagnosis of bovine Chediak-Higashi syndrome.
ACCESSION   E36547
VERSION     E36547.1  GI:18626484
KEYWORDS    JP 2000189165-A/34.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Yamaguchi,H., Kashiguwa,A., Sugimoto,Y. and Tahara,N.
  TITLE     Method of gene diagnosis of bovine Chediak-Higashi syndrome
```

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  JOURNAL   Patent: JP 2000189165-A 34 11-JUL-2000;
            KAGOSHIMA PREF,LIVESTOCK TECHNOLOGY ASSOCIATION
COMMENT     OS   Artificial Sequence
            PN   JP 2000189165-A/34
            PD   11-JUL-2000
            PF   25-DEC-1998 JP 1998368649
            PR
            PI   HIROSHI YAMAGUCHI,AGABA KASHIGUWA,YOSHINORI SUGIMOTO, PI
            NORIO TAHARA
            PC   C12N15/09,C12Q1/68//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,
            PC   C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
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                     /db_xref="taxon:32630"
BASE COUNT        8 a      1 c      8 g      6 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         15 TAGGAGGAT 23


RESULT 10
E40169
LOCUS       E40169                    23 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genetic diagnosis method of bovine Chediak-Higashi syndrome.
ACCESSION   E40169
VERSION     E40169.1  GI:18627243
KEYWORDS    JP 2000189176-A/34.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Yamaguchi,H., Kashiguwa,A., Sugimoto,Y. and Tahara,N.
  TITLE     Genetic diagnosis method of bovine Chediak-Higashi syndrome
  JOURNAL   Patent: JP 2000189176-A 34 11-JUL-2000;
            KAGOSHIMA PREF,LIVESTOCK TECHNOLOGY ASSOCIATION
COMMENT     OS   Artificial Sequence
            PN   JP 2000189176-A/34
            PD   11-JUL-2000
            PF   15-OCT-1999 JP 1999294619
            PR
            PI   HIROSHI YAMAGUCHI,AGABA KASHIGUWA,YOSHINORI SUGIMOTO, PI
            NORIO TAHARA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      1 c      8 g      6 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         15 TAGGAGGAT 23


RESULT 11
DOGC00506A/c
LOCUS       DOGC00506A                23 bp    DNA     linear   STS 11-APR-1996
DEFINITION  Canis familiaris STS microsatellite marker (repeat motif in
            reference clone (GT)2A(GT)9) DNA, sequence tagged site.
ACCESSION   L77541
VERSION     L77541.1  GI:1261665
KEYWORDS    STS; PCR identification; microsatellite; sequence tagged site.
SOURCE      Canis familiaris female adult peripheral blood DNA.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Yuzbasiyan-Gurkan,V., Cao,Y., Gurkan,M., Yuxun,W., Venta,P.J.,
            Brewer,G.J. and Blanton,S.H.
  TITLE     Microsatelite markers for the canine genome
  JOURNAL   Unpublished (1996)
COMMENT     Hotstart, touchdown PCR. Starting at 60 C, decreasing by one degree
            for 10 cycles,  25 further cylces at  52.  Motif and size of
            product as found in the reference dog.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
                     /sex="female"
                     /cell_type="white blood cells"
                     /tissue_type="peripheral blood"
                     /dev_stage="adult"
     STS             1. .23
                     /note="product size 173"
BASE COUNT        6 a      9 c      0 g      8 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         16 TAGGAGGAT 8


RESULT 12
AR135197/c
LOCUS       AR135197                  24 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 15 from patent US 6194559.
ACCESSION   AR135197
VERSION     AR135197.1  GI:14124102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,S.Young.
  TITLE     Abscisic acid responsive element-binding transcription factors
  JOURNAL   Patent: US 6194559-A 15 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      8 t
ORIGIN

  Query Match             100.0%;  Score 9;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 13
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```
AR146693/c
LOCUS       AR146693                 24 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 15 from patent US 6218527.
ACCESSION   AR146693
VERSION     AR146693.1  GI:15109882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,S.Young.
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 3
  JOURNAL   Patent: US 6218527-A 15 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      8 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 14
AR152264/c
LOCUS       AR152264                 24 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 15 from patent US 6232461.
ACCESSION   AR152264
VERSION     AR152264.1  GI:15118314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,S.Young.
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding ractor 4
  JOURNAL   Patent: US 6232461-A 15 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      8 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


RESULT 15
AR157802/c
LOCUS       AR157802                 24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 15 from patent US 6245905.
ACCESSION   AR157802
VERSION     AR157802.1  GI:16218814
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,S.Young.
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 2
  JOURNAL   Patent: US 6245905-A 15 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      8 t
ORIGIN

  Query Match           100.0%;  Score 9;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAGGAGGAT 9
              |||||||||
Db         17 TAGGAGGAT 9


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GenCore version 5.1.6

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Perfect score: 11
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: gb_htg:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	11	100.0	11	6	AR016034	AR016034 Sequence
2	11	100.0	11	6	AR026486	AR026486 Sequence
c 3	11	100.0	11	6	AR026487	AR026487 Sequence
c 4	11	100.0	11	6	AR059195	AR059195 Sequence
c 5	11	100.0	11	6	AR075506	AR075506 Sequence
c 6	11	100.0	11	6	AR161904	AR161904 Sequence
c 7	11	100.0	11	6	AX033373	AX033373 Sequence
8	11	100.0	11	6	AX268757	AX268757 Sequence
c 9	11	100.0	11	6	AX268761	AX268761 Sequence
10	11	100.0	11	6	AX283296	AX283296 Sequence
c 11	11	100.0	11	6	I31749	I31749 Sequence 2
c 12	11	100.0	15	6	AR026479	AR026479 Sequence
c 13	11	100.0	16	6	AR050942	AR050942 Sequence
c 14	11	100.0	16	6	AR204610	AR204610 Sequence
c 15	11	100.0	16	6	I51743	I51743 Sequence 11
16	11	100.0	17	6	A84605	A84605 Sequence 15
17	11	100.0	17	6	AR026488	AR026488 Sequence
c 18	11	100.0	17	6	AR145675	AR145675 Sequence
c 19	11	100.0	17	6	AR145676	AR145676 Sequence
20	11	100.0	18	6	A79654	A79654 Sequence 3
c 21	11	100.0	18	6	A79665	A79665 Sequence 14
22	11	100.0	18	6	A84598	A84598 Sequence 8
c 23	11	100.0	18	6	A84599	A84599 Sequence 9
24	11	100.0	18	6	AR016059	AR016059 Sequence
25	11	100.0	18	6	AR026482	AR026482 Sequence
26	11	100.0	18	6	AR026483	AR026483 Sequence
c 27	11	100.0	18	6	AR026484	AR026484 Sequence
28	11	100.0	18	6	AR037860	AR037860 Sequence
29	11	100.0	18	6	AR037861	AR037861 Sequence
c 30	11	100.0	18	6	AR037862	AR037862 Sequence
31	11	100.0	18	6	AR050936	AR050936 Sequence
32	11	100.0	18	6	AR050962	AR050962 Sequence
33	11	100.0	18	6	AR053263	AR053263 Sequence
34	11	100.0	18	6	AR054739	AR054739 Sequence
35	11	100.0	18	6	AR054740	AR054740 Sequence
c 36	11	100.0	18	6	AR054741	AR054741 Sequence
c 37	11	100.0	18	6	AR059509	AR059509 Sequence
c 38	11	100.0	18	6	AR059546	AR059546 Sequence
39	11	100.0	18	6	AR059547	AR059547 Sequence
40	11	100.0	18	6	AR069393	AR069393 Sequence
41	11	100.0	18	6	AR069394	AR069394 Sequence
c 42	11	100.0	18	6	AR069395	AR069395 Sequence
43	11	100.0	18	6	AR075504	AR075504 Sequence
44	11	100.0	18	6	AR079895	AR079895 Sequence
c 45	11	100.0	18	6	AR079896	AR079896 Sequence

ALIGNMENTS

RESULT 1
AR016034/c
LOCUS AR016034 11 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776679.
ACCESSION AR016034
VERSION AR016034.1 GI:3972311
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 2 07-JUL-1998;
FEATURES Location/Qualifiers

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     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 2
AR026486
LOCUS       AR026486                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5856096.
ACCESSION   AR026486
VERSION     AR026486.1  GI:5937326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 11 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        2 a      0 c      5 g      4 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db          1 GTTAGGGTTAG 11


RESULT 3
AR026487/c
LOCUS       AR026487                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5856096.
ACCESSION   AR026487
VERSION     AR026487.1  GI:5937327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 12 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 4
AR059195/c
LOCUS       AR059195                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5837857.
ACCESSION   AR059195
VERSION     AR059195.1  GI:5984772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5837857-A 2 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 5
AR075506/c
LOCUS       AR075506                  11 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 3 from patent US 5958680.
ACCESSION   AR075506
VERSION     AR075506.1  GI:10002256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5958680-A 3 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 6
AR161904/c
LOCUS       AR161904                  11 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 2 from patent US 6258535.
ACCESSION   AR161904
VERSION     AR161904.1  GI:16228913
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 6258535-A 2 10-JUL-2001;
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FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 7
AX033373/c
LOCUS       AX033373                 11 bp    mRNA    linear   PAT 21-SEP-2000
DEFINITION  Sequence 5 from Patent WO0046601.
ACCESSION   AX033373
VERSION     AX033373.1  GI:10280147
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Larsen,F. and Skaanseng,M.
  TITLE     Detecting telomerase activity
  JOURNAL   Patent: WO 0046601-A 5 10-AUG-2000;
            LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 8
AX268757
LOCUS       AX268757                 11 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 5 from Patent WO0174342.
ACCESSION   AX268757
VERSION     AX268757.1  GI:16541829
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 5 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        2 a      0 c      5 g      4 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||||
Db          1 GTTAGGGTTAG 11


RESULT 9
AX268761/c
LOCUS       AX268761                 11 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 9 from Patent WO0174342.
ACCESSION   AX268761
VERSION     AX268761.1  GI:16541833
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gilchrest,B.A., Yaar,M. and Eller,M.
  TITLE     Use of locally applied dna fragments
  JOURNAL   Patent: WO 0174342-A 9 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Fragment"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 10
AX283296
LOCUS       AX283296                 11 bp    DNA     linear   PAT 20-NOV-2001
DEFINITION  Sequence 60 from Patent WO0179249.
ACCESSION   AX283296
VERSION     AX283296.1  GI:17044177
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives, agents and methods for
            producing the same
  JOURNAL   Patent: WO 0179249-A 60 25-OCT-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz:
                     Oligonukleotide"
BASE COUNT        2 a      0 c      5 g      4 t
ORIGIN

  Query Match             100.0%;  Score 11;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||||
Db          1 GTTAGGGTTAG 11


RESULT 11
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I31749/c
LOCUS       I31749                  11 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5583016.
ACCESSION   I31749
VERSION     I31749.1  GI:1822540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5583016-A 2 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
BASE COUNT        4 a      5 c      0 g      2 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.5e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         11 GTTAGGGTTAG 1


RESULT 12
AR026479/c
LOCUS       AR026479                15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5856096.
ACCESSION   AR026479
VERSION     AR026479.1  GI:5937319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
  TITLE     Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
  JOURNAL   Patent: US 5856096-A 4 05-JAN-1999;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        4 a      9 c      0 g      2 t
ORIGIN

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Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3


RESULT 13
AR050942/c
LOCUS       AR050942                16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5830644.
ACCESSION   AR050942
VERSION     AR050942.1  GI:5974306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Shay,J. and Wright,W.E.
  TITLE     Method for screening for agents which increase telomerase activity
            in a cell
  JOURNAL   Patent: US 5830644-A 11 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        4 a      9 c      0 g      3 t
ORIGIN

  Query Match           100.0%;  Score 11;  DB 6;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 2.3e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3


RESULT 14
AR204610/c
LOCUS       AR204610                16 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 60 from patent US 6368789.
ACCESSION   AR204610
VERSION     AR204610.1  GI:21501980
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
  TITLE     Screening methods to identify inhibitors of telomerase activity
  JOURNAL   Patent: US 6368789-A 60 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        4 a      9 c      0 g      3 t
ORIGIN

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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3


RESULT 15
I51743/c
LOCUS       I51743                  16 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 11 from patent US 5645986.
ACCESSION   I51743
VERSION     I51743.1  GI:2472944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
            Wright,W.E., Blackburn,E.H. and Vaziri,H.
  TITLE     Therapy and diagnosis of conditions related to telomere length
            and/or telomerase activity
  JOURNAL   Patent: US 5645986-A 11 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .16
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BASE COUNT        4 a      9 c      0 g      3 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.3e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTAGGGTTAG 11
              ||||||||||
Db         13 GTTAGGGTTAG 3
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GenCore version 5.1.6

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Title: US-09-540-843-3
Perfect score: 7
Sequence: 1 agtatga 7

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Searched: 845702 seqs, 674182571 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	7	100.0	7	9	US-10-122-630-3	Sequence 3, Appli
	2	7	100.0	7	9	US-10-122-630-7	Sequence 7, Appli
	3	7	100.0	7	9	US-10-122-633-3	Sequence 3, Appli
	4	7	100.0	7	9	US-10-122-633-7	Sequence 7, Appli
	5	7	100.0	9	9	US-10-122-630-1	Sequence 1, Appli
	6	7	100.0	9	9	US-10-122-633-1	Sequence 1, Appli
	7	7	100.0	10	10	US-09-398-399-31	Sequence 31, Appl
	8	7	100.0	10	10	US-09-899-381-31	Sequence 31, Appl
c	9	7	100.0	10	12	US-10-033-145-1423	Sequence 1423, Ap
c	10	7	100.0	14	9	US-09-875-440-22	Sequence 22, Appl
	11	7	100.0	15	10	US-09-504-231A-527	Sequence 527, App
	12	7	100.0	15	10	US-09-504-231A-528	Sequence 528, App
	13	7	100.0	15	10	US-09-504-231A-529	Sequence 529, App
c	14	7	100.0	15	10	US-09-504-231A-1527	Sequence 1527, Ap
c	15	7	100.0	15	10	US-09-504-231A-1569	Sequence 1569, Ap
c	16	7	100.0	15	10	US-09-504-231A-1570	Sequence 1570, Ap
	17	7	100.0	15	10	US-09-398-399-30	Sequence 30, Appl
	18	7	100.0	15	10	US-09-899-381-30	Sequence 30, Appl
	19	7	100.0	15	10	US-09-274-553D-527	Sequence 527, App
	20	7	100.0	15	10	US-09-274-553D-528	Sequence 528, App
	21	7	100.0	15	10	US-09-274-553D-529	Sequence 529, App
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c	23	7	100.0	15	10	US-09-274-553D-1569	Sequence 1569, Ap
c	24	7	100.0	15	10	US-09-274-553D-1570	Sequence 1570, Ap
c	25	7	100.0	15	10	US-09-272-343-1	Sequence 1, Appli
	26	7	100.0	15	10	US-09-272-343-2	Sequence 2, Appli
	27	7	100.0	17	9	US-10-060-830-716	Sequence 716, App
	28	7	100.0	17	9	US-10-060-830-717	Sequence 717, App
	29	7	100.0	17	9	US-10-060-830-718	Sequence 718, App
	30	7	100.0	17	9	US-10-060-830-719	Sequence 719, App
	31	7	100.0	17	9	US-10-060-830-720	Sequence 720, App
	32	7	100.0	17	9	US-10-060-830-721	Sequence 721, App
	33	7	100.0	17	9	US-10-060-830-722	Sequence 722, App
	34	7	100.0	17	9	US-10-060-830-723	Sequence 723, App
	35	7	100.0	17	9	US-10-060-830-724	Sequence 724, App
	36	7	100.0	17	9	US-10-060-830-725	Sequence 725, App
	37	7	100.0	17	9	US-10-060-830-726	Sequence 726, App
	38	7	100.0	17	9	US-09-818-875-639	Sequence 639, App
c	39	7	100.0	17	9	US-09-818-875-640	Sequence 640, App
	40	7	100.0	17	9	US-09-848-754A-443	Sequence 443, App
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	43	7	100.0	17	9	US-09-848-754A-2584	Sequence 2584, Ap
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ALIGNMENTS

RESULT 1
US-10-122-630-3
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3

Query Match 100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGTATGA 7
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Db          1 AGTATGA 7
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RESULT 2
US-10-122-630-7
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

  Query Match             100.0%;  Score 7;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
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Db          1 AGTATGA 7


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; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

  Query Match             100.0%;  Score 7;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 4
US-10-122-633-7
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-019
;  CURRENT APPLICATION NUMBER: US/10/122,633
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

  Query Match             100.0%;  Score 7;  DB 9;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 5
US-10-122-630-1
; Sequence 1, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
;  APPLICANT: Gilchrest, Barbara A.
;  APPLICANT:  Eller, Mark S.
;  APPLICANT:  Yaar, Mina
;  TITLE OF INVENTION: Method to Inhibit Cell Growth Using
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: 0054.1088-018
;  CURRENT APPLICATION NUMBER: US/10/122,630
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 08/467,012
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US96/08386
;  PRIOR FILING DATE: 1996-06-03
;  PRIOR APPLICATION NUMBER: US 09/048,927
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/540,843
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10162
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1
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Query Match 100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8
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RESULT 6
US-10-122-633-1
; Sequence 1, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

Query Match 100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8
```

RESULT 7
US-09-398-399-31
; Sequence 31, Application US/09398399
; Patent No. US20020051973A1
; GENERAL INFORMATION:
; APPLICANT: DELENSTARR, GLENDA C.
; APPLICANT: LEFKOWITZ, STEVEN M.
; APPLICANT: LUEBKE, KEVIN J.
; APPLICANT: OVERMAN, LESLIE B.
; APPLICANT: SAMPRAS, NICHOLAS M.
; APPLICANT: SAMPSON, JEFFREY R.
; APPLICANT: WOLBER, PAUL K.
; TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC
; TITLE OF INVENTION: ACIDS TO SURFACES
; FILE REFERENCE: 10981620-1
; CURRENT APPLICATION NUMBER: US/09/398,399
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-31

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7
```

RESULT 8
US-09-899-381-31
; Sequence 31, Application US/09899381
; Patent No. US20020068293A1
; GENERAL INFORMATION:
; APPLICANT: Delenstarr, Glend C.
; APPLICANT: Wolber, Pual K.
; APPLICANT: Sana, Theodore R.
; TITLE OF INVENTION: Arrays Having Background Features and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: 10010760-1
; CURRENT APPLICATION NUMBER: US/09/899,381
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/398,399
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic probe
US-09-899-381-31

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7
```

RESULT 9
US-10-033-145-1423/c
; Sequence 1423, Application US/10033145
; Patent No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1423
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1423

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db          7 AGTATGA 1
```

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RESULT 10
US-09-875-440-22/c
; Sequence 22, Application US/09875440
; Patent No. US20020156035A1
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT:  Jefferson, Anne B.
;  APPLICANT:  Winter, Jill A.
;  APPLICANT:  Randazzo, Filippo
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  NEOPLASTIC DISEASE USING NET-4 MODULATORS
;  FILE REFERENCE: PP-01701.002/200130.522
;  CURRENT APPLICATION NUMBER: US/09/875,440
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-situ
;   OTHER INFORMATION: hybridization
US-09-875-440-22

  Query Match             100.0%;  Score 7;  DB 9;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+04;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         13 AGTATGA 7


RESULT 11
US-09-504-231A-527
; Sequence 527, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-527

  Query Match             100.0%;  Score 7;  DB 10;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 4.9e+04;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          9 AGUAUGA 15


RESULT 12
US-09-504-231A-528
; Sequence 528, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 528
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-528

  Query Match             100.0%;  Score 7;  DB 10;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 4.9e+04;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          8 AGUAUGA 14


RESULT 13
US-09-504-231A-529
; Sequence 529, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 529
;   LENGTH: 15
```

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-529

Query Match 100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 71.4%; Pred. No. 4.9e+04;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              ||:|:||
Db          5 AGUAUGA 11
```

RESULT 14
US-09-504-231A-1527/c
; Sequence 1527, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1527
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1527

Query Match 100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db         13 AGTATGA 7
```

RESULT 15
US-09-504-231A-1569/c
; Sequence 1569, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1569
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1569

Query Match 100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGTATGA 7
              |||||||
Db         12 AGTATGA 6
```

Search completed: June 2, 2003, 23:43:13
Job time : 50.6829 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:31:20 ; Search time 28.6829 Seconds
(without alignments)
74.844 Million cell updates/sec

Title: US-09-540-843-3
Perfect score: 7
Sequence: 1 agtatga 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	7	100.0	7	3	US-09-048-927-3	Sequence 3, Appli
	2	7	100.0	9	3	US-09-048-927-1	Sequence 1, Appli
	3	7	100.0	14	2	US-08-485-133-27	Sequence 27, Appl
c	4	7	100.0	14	2	US-08-744-905A-4	Sequence 4, Appli
	5	7	100.0	15	1	US-08-334-847-24	Sequence 24, Appl
	6	7	100.0	15	1	US-08-334-847-327	Sequence 327, App
c	7	7	100.0	15	1	US-08-671-071B-2	Sequence 2, Appli
c	8	7	100.0	15	2	US-08-747-121-4	Sequence 4, Appli
	9	7	100.0	15	2	US-08-585-684B-130	Sequence 130, App
	10	7	100.0	15	2	US-08-585-684B-1315	Sequence 1315, Ap
	11	7	100.0	15	2	US-08-485-133-28	Sequence 28, Appl
c	12	7	100.0	15	3	US-09-094-714A-33	Sequence 33, Appl
c	13	7	100.0	15	3	US-09-094-714A-34	Sequence 34, Appl
c	14	7	100.0	15	4	US-09-049-190-6	Sequence 6, Appli
c	15	7	100.0	15	4	US-09-049-190-7	Sequence 7, Appli
	16	7	100.0	15	4	US-09-038-073-130	Sequence 130, App
	17	7	100.0	15	4	US-09-038-073-1315	Sequence 1315, Ap
c	18	7	100.0	15	4	US-08-932-140C-6	Sequence 6, Appli
c	19	7	100.0	15	4	US-08-932-140C-7	Sequence 7, Appli
c	20	7	100.0	15	4	US-09-253-977-2	Sequence 2, Appli
c	21	7	100.0	16	1	US-07-977-284A-59	Sequence 59, Appl
	22	7	100.0	16	1	US-08-719-593-24	Sequence 24, Appl
c	23	7	100.0	16	2	US-08-256-426B-59	Sequence 59, Appl
	24	7	100.0	16	3	US-08-458-814-1	Sequence 1, Appli
	25	7	100.0	17	1	US-08-390-850-461	Sequence 461, App
	26	7	100.0	17	1	US-08-435-634-461	Sequence 461, App
c	27	7	100.0	17	1	US-08-758-306-365	Sequence 365, App
c	28	7	100.0	17	1	US-08-758-306-367	Sequence 367, App
c	29	7	100.0	17	1	US-08-758-306-369	Sequence 369, App
c	30	7	100.0	17	1	US-08-758-306-371	Sequence 371, App
c	31	7	100.0	17	1	US-08-758-306-813	Sequence 813, App
c	32	7	100.0	17	1	US-08-758-306-815	Sequence 815, App
c	33	7	100.0	17	2	US-08-671-320-6	Sequence 6, Appli
c	34	7	100.0	17	2	US-08-868-577-6	Sequence 6, Appli
	35	7	100.0	17	2	US-08-485-133-2	Sequence 2, Appli
	36	7	100.0	17	3	US-08-985-162-443	Sequence 443, App
	37	7	100.0	17	3	US-08-985-162-444	Sequence 444, App
	38	7	100.0	18	1	US-07-688-352C-8	Sequence 8, Appli
	39	7	100.0	18	1	US-08-363-585-55	Sequence 55, Appl
	40	7	100.0	18	1	US-08-358-995-10	Sequence 10, Appl
c	41	7	100.0	18	2	US-08-928-692-48	Sequence 48, Appl
	42	7	100.0	18	2	US-08-474-379C-8	Sequence 8, Appli
	43	7	100.0	18	2	US-09-200-141-19	Sequence 19, Appl
	44	7	100.0	18	2	US-09-213-768-24	Sequence 24, Appl
	45	7	100.0	18	2	US-09-213-768-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-048-927-3
; Sequence 3, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-3

Query Match 100.0%; Score 7; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+07;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7
```

RESULT 2
US-09-048-927-1
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012

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;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Fragment
US-09-048-927-1

  Query Match             100.0%;  Score 7;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8


RESULT 3
US-08-485-133-27
; Sequence 27, Application US/08485133
; Patent No. 5976789
;  GENERAL INFORMATION:
;    APPLICANT:  Allibert, Patrice A.
;    APPLICANT:  Cros, Philippe
;    APPLICANT:  Mach, Bernard F.
;    APPLICANT:  Mandrand, Bernard F.
;    APPLICANT:  Tiercy, Jean-Marie
;    TITLE OF INVENTION:  SYSTEM OF PROBES ENABLING HLA-DR TYPING
;    TITLE OF INVENTION:  TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. Box 19928
;      CITY:  Alexandria
;      STATE:  Virginia
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,133
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,143
;      FILING DATE:  11-MAR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 28596A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-485-133-27

  Query Match             100.0%;  Score 7;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          8 AGTATGA 14


RESULT 4
US-08-744-905A-4/c
; Sequence 4, Application US/08744905A
; Patent No. 5990294
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Gerald
;    APPLICANT:  Boynton, Alton
;    APPLICANT:  Sehgal, Anil
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID
;    TITLE OF INVENTION:  SEQUENCES OF C4-2, A TUMOR SUPPRESSOR GENE,
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,905A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baldwin, Geraldine F
;      REGISTRATION NUMBER:  31,232
;      REFERENCE/DOCKET NUMBER:  8511-009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)7909090
;      TELEFAX:  (212)8698864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified Base
;      LOCATION:  1
;      OTHER INFORMATION:  Where N is any nucleotide
US-08-744-905A-4

  Query Match             100.0%;  Score 7;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         14 AGTATGA 8


RESULT 5
US-08-334-847-24
; Sequence 24, Application US/08334847
; Patent No. 5693532
;  GENERAL INFORMATION:
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  Pavco, Pam
;    APPLICANT:  Woolf, Tod
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
```

```
;    TITLE OF INVENTION:  INHIBITING RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS
;    NUMBER OF SEQUENCES:  909
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/334,847
;      FILING DATE:  No. 5693532ember 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-334-847-24

  Query Match             100.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 6.1e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          5 AGUAUGA 11


RESULT 6
US-08-334-847-327
; Sequence 327, Application US/08334847
; Patent No. 5693532
;  GENERAL INFORMATION:
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  Pavco, Pam
;    APPLICANT:  Woolf, Tod
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS
;    NUMBER OF SEQUENCES:  909
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/334,847
;      FILING DATE:  No. 5693532ember 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  327:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-334-847-327

  Query Match             100.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 6.1e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          5 AGUAUGA 11


RESULT 7
US-08-671-071B-2/c
; Sequence 2, Application US/08671071B
; Patent No. 5811270
;  GENERAL INFORMATION:
;    APPLICANT:  Grandgenett, Duane
;    TITLE OF INVENTION:  An in vitro method for concerted integration of
;    TITLE OF INVENTION:  donor DNA molecules using retroviral integrase proteins.
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Grandgenett, Duane
;      STREET:  8610 Henrietta Ave
;      CITY:  Brentwood
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Distette, 3.5 inch;
;      COMPUTER:  Gateway 2000,4DX2-66E(Intel)
;      OPERATING SYSTEM:  IBM clone
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/671,071B
;      FILING DATE:  06/27/96
;      CLASSIFICATION:  435
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 962-0064
;      TELEFAX:  (314) 577-8406
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:  Combination of avian or HIV-1 retrovirus
;    ORIGINAL SOURCE:  DNA, piAN7 plasmid and pGEM plasmid.
;    IMMEDIATE SOURCE:  Same as in 2,vi.
```

```
;    FEATURE:
;      OTHER INFORMATION:  The sequence is the bottom strand of
;      OTHER INFORMATION:  M-2 U5 and the pGEM target of the top clone shown in
;      OTHER INFORMATION:  Figure 14 of original application.
US-08-671-071B-2

  Query Match           100.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 3


RESULT 8
US-08-747-121-4/c
; Sequence 4, Application US/08747121
; Patent No. 5874290
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Gerald
;    APPLICANT:  Boynton, Alton
;    APPLICANT:  Sehgal, Anil
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID
;    TITLE OF INVENTION:  SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
;    TITLE OF INVENTION:  BRAIN TUMORS AND METHODS BASED THEREON
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/747,121
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baldwin, Geraldine F
;      REGISTRATION NUMBER:  31,232
;      REFERENCE/DOCKET NUMBER:  8511-008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)7909090
;      TELEFAX:  (212)8698864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified Base
;      LOCATION:  1
;      OTHER INFORMATION:  Where N is any nucleotide
US-08-747-121-4

  Query Match           100.0%;  Score 7;  DB 2;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         15 AGTATGA 9


RESULT 9
US-08-585-684B-130
; Sequence 130, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-130

  Query Match           100.0%;  Score 7;  DB 2;  Length 15;
  Best Local Similarity  71.4%;  Pred. No. 6.1e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          5 AGUAUGA 11


RESULT 10
US-08-585-684B-1315
; Sequence 1315, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
```

```
;       STREET:  633 West Fifth Street
;       STREET:  Suite 4700
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/585,684B
;       FILING DATE:  January 16, 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/000,951
;       FILING DATE:  July 7, 1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  218/078
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1315:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-585-684B-1315

  Query Match             100.0%;  Score 7;  DB 2;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 6.1e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              ||:|:||
Db          5 AGUAUGA 11


RESULT 11
US-08-485-133-28
; Sequence 28, Application US/08485133
; Patent No. 5976789
;  GENERAL INFORMATION:
;    APPLICANT:  Allibert, Patrice A.
;    APPLICANT:  Cros, Philippe
;    APPLICANT:  Mach, Bernard F.
;    APPLICANT:  Mandrand, Bernard F.
;    APPLICANT:  Tiercy, Jean-Marie
;    TITLE OF INVENTION:  SYSTEM OF PROBES ENABLING HLA-DR TYPING
;    TITLE OF INVENTION:  TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. Box 19928
;      CITY:  Alexandria
;      STATE:  Virginia
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,133
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,143
;      FILING DATE:  11-MAR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 28596A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-485-133-28

  Query Match             100.0%;  Score 7;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 15


RESULT 12
US-09-094-714A-33/c
; Sequence 33, Application US/09094714A
; Patent No. 6117847
;  GENERAL INFORMATION:
;    APPLICANT:  C. Frank Bennett, Nicholas M. Dean
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
;    TITLE OF INVENTION:  PROTEIN KINASE C EXPRESSION
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,714A
;      FILING DATE:  June 15, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/601,269
;      FILING DATE:  14-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/478,178
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/089,996
;      FILING DATE:  09-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/852,852
;      FILING DATE:  16-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  ISIS-2943
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-094-714A-33

  Query Match             100.0%;  Score 7;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         12 AGTATGA 6


RESULT 13
US-09-094-714A-34/c
; Sequence 34, Application US/09094714A
; Patent No. 6117847
;  GENERAL INFORMATION:
;    APPLICANT:  C. Frank Bennett, Nicholas M. Dean
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
;    TITLE OF INVENTION:  PROTEIN KINASE C EXPRESSION
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,714A
;      FILING DATE:  June 15, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/601,269
;      FILING DATE:  14-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/478,178
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/089,996
;      FILING DATE:  09-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/852,852
;      FILING DATE:  16-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  ISIS-2943
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-094-714A-34

  Query Match             100.0%;  Score 7;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         14 AGTATGA 8


RESULT 14
US-09-049-190-6/c
; Sequence 6, Application US/09049190
; Patent No. 6190866
;  GENERAL INFORMATION:
;    APPLICANT:  Nielsen et al.
;    TITLE OF INVENTION:  Peptide Nucleic Acids Having
;    TITLE OF INVENTION:  Antibacterial Activity
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz          & No. 6190866ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,190
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John W. Caldwell
;      REGISTRATION NUMBER:  28,937
;      REFERENCE/DOCKET NUMBER:  ISIS-2560
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
```

```
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
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;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
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;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
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;      OTHER INFORMATION:  backbone
US-09-049-190-6

  Query Match             100.0%;  Score 7;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         10 AGTATGA 4


RESULT 15
US-09-049-190-7/c
; Sequence 7, Application US/09049190
; Patent No. 6190866
;  GENERAL INFORMATION:
;    APPLICANT:  Nielsen et al.
;    TITLE OF INVENTION:  Peptide Nucleic Acids Having
;    TITLE OF INVENTION:  Antibacterial Activity
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz          & No. 6190866ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,190
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John W. Caldwell
;      REGISTRATION NUMBER:  28,937
;      REFERENCE/DOCKET NUMBER:  ISIS-2560
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;      OTHER INFORMATION:  backbone
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
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;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  12
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  13
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  14
;       OTHER INFORMATION:  N-acetyl(2-aminoethyl)glycine
;       OTHER INFORMATION:  backbone
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  N-[acetyl(2-aminoethyl)]-C-lysine-glycine
;       OTHER INFORMATION:  backbone
US-09-049-190-7

  Query Match             100.0%;  Score 7;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         13 AGTATGA 7


Search completed: June  2, 2003, 20:38:33
Job time : 29.6829 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 18:29:55 ; Search time 878.415 Seconds
(without alignments)
129.060 Million cell updates/sec

Title: US-09-540-843-3
Perfect score: 7
Sequence: 1 agtatga 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		7	100.0	19	17	AZ817238	AZ817238 2M0086E01
c 2		7	100.0	19	17	AZ990856	AZ990856 2M0274F14
c 3		7	100.0	22	17	AZ623945	AZ623945 1M0462J10
4		7	100.0	22	17	AZ658158	AZ658158 1M0534H17
c 5		7	100.0	24	10	AW059679	AW059679 AHuTH.bss
c 6		7	100.0	24	17	AZ423817	AZ423817 1M0203P19
c 7		7	100.0	24	17	AZ478673	AZ478673 1M0298J20
c 8		7	100.0	24	17	AZ816657	AZ816657 2M0085E05
c 9		7	100.0	25	14	H96935	H96935 yu01d01.r1
c 10		7	100.0	25	17	AZ605844	AZ605844 1M0427J22
c 11		7	100.0	25	17	AZ802490	AZ802490 2M0061I22
12		7	100.0	25	17	BH852860	BH852860 SALK_0756
13		7	100.0	25	17	BH852866	BH852866 SALK_0756
c 14		7	100.0	25	17	BH857761	BH857761 SALK_0156
c 15		7	100.0	26	17	AZ345685	AZ345685 1M0080C06
c 16		7	100.0	26	17	AZ473354	AZ473354 1M0289N08
c 17		7	100.0	27	14	D45824	D45824 HUMGS03044
18		7	100.0	27	17	TA187C01P	AL477519 T. brucei
c 19		7	100.0	28	9	AI790546	AI790546 ul02e08.x
20		7	100.0	28	17	AZ861130	AZ861130 2M0167M21
c 21		7	100.0	29	17	BH856420	BH856420 SALK_0797
c 22		7	100.0	29	17	TA230F03P	AL481025 T. brucei
c 23		7	100.0	30	14	C21099	C21099 HUMGS000262
24		7	100.0	30	17	AL766985	AL766985 Arabidops
25		7	100.0	31	9	AI159285	AI159285 vz85b12.r
c 26		7	100.0	31	9	AI198585	AI198585 qf50c03.x
27		7	100.0	31	17	BH853749	BH853749 SALK_0782
28		7	100.0	32	17	AZ587241	AZ587241 1M0394D14
c 29		7	100.0	32	17	BH862820	BH862820 SALK_0906
c 30		7	100.0	32	17	AL769600	AL769600 Arabidops
31		7	100.0	33	17	AZ463054	AZ463054 1M0271H10
32		7	100.0	33	17	AZ481169	AZ481169 1M0303D13
c 33		7	100.0	33	17	AZ778279	AZ778279 2M0013N15
c 34		7	100.0	33	17	AZ826520	AZ826520 2M0102B04
35		7	100.0	33	17	TA307A09Q	AL488827 T. brucei
36		7	100.0	34	9	AU256929	AU256929 AU256929
c 37		7	100.0	34	17	AZ333219	AZ333219 1M0062O09
38		7	100.0	35	17	AZ476942	AZ476942 1M0296H11
39		7	100.0	35	17	AZ817309	AZ817309 2M0086N18
40		7	100.0	36	9	AU258145	AU258145 AU258145
41		7	100.0	36	9	AA624760	AA624760 vn91a08.r
c 42		7	100.0	36	17	AZ405651	AZ405651 1M0174O03
c 43		7	100.0	36	17	AZ621129	AZ621129 1M0454I08
44		7	100.0	36	17	AZ776722	AZ776722 2M0010A12
c 45		7	100.0	36	17	BH789482	BH789482 SALK_0297

ALIGNMENTS

RESULT 1
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LOCUS AZ817238 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0086E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086E01 R, DNA sequence.
ACCESSION AZ817238
VERSION AZ817238.1 GI:12987146
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0086 row: E column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086E01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 1 c 6 g 6 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 10 AGTATGA 16

RESULT 2
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LOCUS AZ990856 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0274F14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0274F14 R, DNA sequence.
ACCESSION AZ990856
VERSION AZ990856.1 GI:13862083
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0274 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0274F14"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 5 c 0 g 6 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 18 AGTATGA 12

RESULT 3
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LOCUS AZ623945 22 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0462J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0462J10 F, DNA sequence.
ACCESSION AZ623945
VERSION AZ623945.1 GI:11746135
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0462 row: J column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0462J10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 8 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 11 AGTATGA 5

RESULT 4
AZ658158
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DEFINITION 1M0534H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0534H17 R, DNA sequence.
ACCESSION AZ658158
VERSION AZ658158.1 GI:11795304
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: H column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0534H17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 0 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 4 AGTATGA 10

RESULT 5
AW059679/c
LOCUS AW059679 24 bp mRNA linear EST 23-AUG-2000
DEFINITION AHuTH.bsst.dnc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW059679
VERSION AW059679.1 GI:6652001
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
MEDLINE 20144098
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate.
High quality sequence stop: 24.

FEATURES Location/Qualifiers

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    source          1. .24
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone_lib="DNC15"
                    /cell_type="monocyctic leukemia"
                    /cell_line="THP-1 (TIB-202)"
                    /note="Vector: pCR2.1; Cloning of PCR products from
                    micro-beads carrying 3' end of down-regulated cDNA. THP-1
                    cells non-induced (treated with DMSO only). "
BASE COUNT        9 a      6 c      1 g      8 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 10;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         23 AGTATGA 17


RESULT 6
AZ423817/c
LOCUS       AZ423817                 24 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0203P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0203P19 F, DNA sequence.
ACCESSION   AZ423817
VERSION     AZ423817.1  GI:10547830
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0203  row: P  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0203P19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      3 c      2 g     12 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 17;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db         17 AGTATGA 11


RESULT 7
AZ478673/c
LOCUS       AZ478673                 24 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0298J20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0298J20 R, DNA sequence.
ACCESSION   AZ478673
VERSION     AZ478673.1  GI:10637794
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0298  row: J  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0298J20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 3 g 7 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 8 AGTATGA 2

RESULT 8
AZ816657/c
LOCUS AZ816657 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0085E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0085E05 R, DNA sequence.
ACCESSION AZ816657
VERSION AZ816657.1 GI:12986565
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: E column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0085E05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 3 g 8 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 19 AGTATGA 13

RESULT 9
H96935/c
LOCUS H96935 25 bp mRNA linear EST 11-DEC-1995
DEFINITION yu01d01.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232513 5' similar to SP:S36112 S36112 RETINOBLASTOMA-BINDING PROTEIN - ;, mRNA sequence.
ACCESSION H96935
VERSION H96935.1 GI:1113978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1325 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/db_xref="GDB:3862504"
/db_xref="taxon:9606"
/clone="IMAGE:232513"
/clone_lib="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCGTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo. "
BASE COUNT 6 a 5 c 6 g 8 t
ORIGIN

Query Match 100.0%; Score 7; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 19 AGTATGA 13

RESULT 10
AZ605844/c
LOCUS AZ605844 25 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0427J22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0427J22 F, DNA sequence.
ACCESSION AZ605844
VERSION AZ605844.1 GI:11728034
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0427 row: J column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0427J22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 7 a 6 c 5 g 7 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 17 AGTATGA 11

RESULT 11
AZ802490/c
LOCUS AZ802490 25 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0061I22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0061I22 F, DNA sequence.
ACCESSION AZ802490
VERSION AZ802490.1 GI:12954813
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0061 row: I column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0061I22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."
BASE COUNT 5 a 6 c 5 g 9 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 22 AGTATGA 16

RESULT 12
BH852860
LOCUS BH852860 25 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_075689.48.55.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_075689.48.55.x, DNA
sequence.
ACCESSION BH852860
VERSION BH852860.1 GI:21423731
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At3g41627.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .25
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_075689.48.55.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 9 a 2 c 6 g 8 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 12 AGTATGA 18

RESULT 13
BH852866
LOCUS BH852866 25 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_075697.38.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_075697.38.25.x, DNA
sequence.
ACCESSION BH852866
VERSION BH852866.1 GI:21423737
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At3g41627.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .25
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_075697.38.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 9 a 2 c 6 g 8 t
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 12 AGTATGA 18

RESULT 14
BH857761/c
LOCUS BH857761 25 bp DNA linear GSS 08-JUL-2002
DEFINITION SALK_015664.41.95.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_015664.41.95.x, DNA
sequence.
ACCESSION BH857761
VERSION BH857761.1 GI:21708582
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)

```
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated intron of At3g22930.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
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                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT        9 a      5 c      0 g     11 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 17;  Length 25;
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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          8 AGTATGA 2


RESULT 15
AZ345685/c
LOCUS       AZ345685                 26 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080C06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080C06 R, DNA sequence.
ACCESSION   AZ345685
VERSION     AZ345685.1  GI:10424922
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0080  row: C  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080C06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      7 c      0 g     12 t
ORIGIN

  Query Match             100.0%;  Score 7;  DB 17;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          9 AGTATGA 3


Search completed: June  2, 2003, 20:35:40
Job time : 881.415 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 17:32:40 ; Search time 116.951 Seconds
(without alignments)
134.791 Million cell updates/sec

Title: US-09-540-843-3
Perfect score: 7
Sequence: 1 agtatga 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	7	100.0	7	20	AAZ10694	Oligonucleotide se
	2	7	100.0	7	23	AAS14907	Melanogenesis asso
	3	7	100.0	7	23	AAS14911	Melanogenesis asso
	4	7	100.0	9	20	AAZ10692	Oligonucleotide se
	5	7	100.0	9	23	AAS14905	Melanogenesis asso
c	6	7	100.0	10	21	AAZ78995	Human dendritic ce
	7	7	100.0	10	21	AAZ86425	Metastatic breast
	8	7	100.0	10	22	AAH32760	LPS activated huma
	9	7	100.0	10	22	AAF38936	Yeast NORF gene SA
	10	7	100.0	10	22	AAF39793	Yeast NORF gene SA
	11	7	100.0	10	22	AAF40876	Yeast NORF gene SA
c	12	7	100.0	10	24	ABK47394	Human PLA2G1B ASO
	13	7	100.0	10	24	AAL41859	Human GCNT1 allele
	14	7	100.0	10	24	AAI67680	Human IL-8 gene po
c	15	7	100.0	10	24	AAI67681	Human IL-8 gene po
	16	7	100.0	10	24	ABL42801	Human maturation/a
	17	7	100.0	11	24	ABQ86727	Human skin stress/
c	18	7	100.0	12	19	AAV40922	Primer E2AHLF:1726
	19	7	100.0	12	20	AAX19080	Oligonucleotide 1
c	20	7	100.0	12	23	ABH67740	Oligonucleotide pr
c	21	7	100.0	12	23	ABH68353	Oligonucleotide pr
	22	7	100.0	12	23	ABH70774	Oligonucleotide pr
	23	7	100.0	12	23	ABH71335	Oligonucleotide pr
c	24	7	100.0	12	23	ABH71445	Oligonucleotide pr
	25	7	100.0	12	23	ABH71785	Oligonucleotide pr
	26	7	100.0	12	23	ABH74658	Oligonucleotide pr
	27	7	100.0	12	23	ABH74660	Oligonucleotide pr
c	28	7	100.0	12	23	ABH75445	Oligonucleotide pr
c	29	7	100.0	12	23	ABH78137	Oligonucleotide pr
	30	7	100.0	12	23	ABH78185	Oligonucleotide pr
	31	7	100.0	12	23	ABH79172	Oligonucleotide pr
	32	7	100.0	12	23	ABH79256	Oligonucleotide pr
	33	7	100.0	12	23	ABH79332	Oligonucleotide pr
	34	7	100.0	12	23	ABH79629	Oligonucleotide pr
	35	7	100.0	12	23	ABH80384	Oligonucleotide pr
c	36	7	100.0	12	23	ABH80608	Oligonucleotide pr
c	37	7	100.0	12	23	ABH80919	Oligonucleotide pr
c	38	7	100.0	12	23	ABH81994	Oligonucleotide pr
c	39	7	100.0	12	23	ABH82603	Oligonucleotide pr
	40	7	100.0	12	23	ABH84469	Oligonucleotide pr
	41	7	100.0	12	23	ABH84470	Oligonucleotide pr
	42	7	100.0	12	23	ABH84926	Oligonucleotide pr
	43	7	100.0	12	23	ABH86238	Oligonucleotide pr
c	44	7	100.0	12	23	ABH87108	Oligonucleotide pr
	45	7	100.0	12	23	ABH87400	Oligonucleotide pr

ALIGNMENTS

RESULT 1
AAZ10694
ID AAZ10694 standard; DNA; 7 BP.
XX
AC AAZ10694;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 1 AGTATGA 7

RESULT 2
AAS14907
ID AAS14907 standard; DNA; 7 BP.
XX
AC AAS14907;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #3.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 36; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell
CC proliferation by treating cells with at least one oligonucleotide, or
CC its fragment. The compounds, which have cytostatic, anti-allergic,
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC DNA repair processes (or a protective response to later exposure to
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC or a tumour necrosis factor inhibitor. Probably they mimic products of
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair to occur before cell division takes place. The method is
CC especially used to treat carcinoma but may also be used to: treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC allergically mediated inflammation (atopic or contact dermatitis,
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #3, a truncated
CC version of the oligonucleotide shown in AAS14906, one of the
CC oligonucleotides used to inhibit mammalian epithelial cell
CC proliferation, described in the method of the invention.
XX
SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 1 AGTATGA 7

RESULT 3
AAS14911
ID AAS14911 standard; DNA; 7 BP.
XX
AC AAS14911;
XX
DT 14-FEB-2002 (first entry)
XX
DE Melanogenesis associated oligonucleotide #7.
XX
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= a
FT /note= "Phosphorylated"
XX
PN WO200174342-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10162.
XX
PR 31-MAR-2000; 2000US-0540843.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrest BA, Yaar M, Eller M;
XX
DR WPI; 2001-626338/72.
XX
PT Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light -
XX
PS Claim 1; Page 38; 74pp; English.
XX
CC The invention describes inhibition of mammalian epithelial cell

```
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #7, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 23;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 4
AAZ10692
ID   AAZ10692 standard; DNA; 9 BP.
XX
AC   AAZ10692;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW   p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW   UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW   atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW   skin cancer; ss.
XX
OS   Synthetic.
XX
PN   GB2336157-A.
XX
PD   13-OCT-1999.
XX
PF   24-MAR-1999;   99GB-0006758.
XX
PR   26-MAR-1998;   98US-0048927.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 1999-543520/46.
XX
PT   DNA fragments useful for increasing p53 activity in a cell and reducing
PT   susceptibility to UV-induced hyperproliferative diseases -
XX
PS   Claim 11; Page 29; 44pp; English.
XX
CC   AAZ10692-97 represent DNA fragments that are used for increasing p53
CC   activity in a cell. The oligonucleotides are are UV mimetics and
CC   protect cells against subsequent exposure to UV-irradiation or
CC   chemicals. The oligonucleotides are useful for increasing p53 activity
CC   in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC   diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC   rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC   and reducing susceptibility to skin cancer.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 20;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8


RESULT 5
AAS14905
ID   AAS14905 standard; DNA; 9 BP.
XX
AC   AAS14905;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Melanogenesis associated oligonucleotide #1.
XX
KW   Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW   immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW   tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW   carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW   conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "Optionally phosphorylated"
XX
PN   WO200174342-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10162.
XX
PR   31-MAR-2000; 2000US-0540843.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Gilchrest BA,  Yaar M,  Eller M;
XX
DR   WPI; 2001-626338/72.
XX
PT   Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT   carcinoma, using specific oligonucleotides that mimic the effects of
PT   ultra-violet light -
XX
PS   Claim 1; Page 36; 74pp; English.
XX
CC   The invention describes inhibition of mammalian epithelial cell
CC   proliferation by treating cells with at least one oligonucleotide, or
CC   its fragment. The compounds, which have cytostatic, anti-allergic,
CC   anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
CC   immunosuppressive activities, function as 'ultra-violet mimics' to induce
CC   DNA repair processes (or a protective response to later exposure to
CC   radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
CC   or a tumour necrosis factor inhibitor. Probably they mimic products of
CC   DNA damage, or processed DNA-damage intermediates, by inducing the p53
CC   pathway, resulting in transient arrest of cell growth, allowing more time
```

```
CC   for DNA repair to occur before cell division takes place. The method is
CC   especially used to treat carcinoma but may also be used to: treat other
CC   hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC   reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
CC   allergically mediated inflammation (atopic or contact dermatitis,
CC   allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
CC   cells caused by radiation or chemicals; increase melanin production
CC   (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
CC   promote apoptosis in epithelial cells that contain damaged DNA. Also
CC   oligonucleotides that contain non-hydrolyzable backbones are used to
CC   inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC   sequence is melanogenesis associated oligonucleotide #1, one of the
CC   oligonucleotides used to inhibit mammalian epithelial cell
CC   proliferation, described in the method of the invention.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 23;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+08;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          2 AGTATGA 8


RESULT 6
AAZ78995/c
ID   AAZ78995 standard; DNA; 10 BP.
XX
AC   AAZ78995;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1423.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 105; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 4 A; 2 C; 1 G; 3 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 21;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+04;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          7 AGTATGA 1


RESULT 7
AAZ86425
ID   AAZ86425 standard; DNA; 10 BP.
XX
AC   AAZ86425;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5659.
XX
```

```
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 208; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 21;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+04;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          4 AGTATGA 10


RESULT 8
AAH32760
ID   AAH32760 standard; cDNA; 10 BP.
XX
AC   AAH32760;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:133.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 10; Page 28; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;

  Query Match             100.0%;  Score 7;  DB 22;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+04;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATGA 7
              |||||||
Db          1 AGTATGA 7


RESULT 9
AAF38936
ID   AAF38936 standard; DNA; 10 BP.
XX
AC   AAF38936;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5675.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
XX
```

PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 202; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 2 AGTATGA 8

RESULT 10
AAF39793
ID AAF39793 standard; DNA; 10 BP.
XX
AC AAF39793;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6532.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 233; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 other;

Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 1 AGTATGA 7

RESULT 11
AAF40876
ID AAF40876 standard; DNA; 10 BP.
XX
AC AAF40876;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7615.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX

PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 272; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 3 AGTATGA 9

RESULT 12
ABK47394/c
ID ABK47394 standard; DNA; 10 BP.
XX
AC ABK47394;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human PLA2G1B ASO primer extension primer 3' end #5.
XX
KW Human; ss; primer; SNP; single nucleotide polymorphism; pancreatitis;
KW pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; gene therapy;
KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening;
KW ASO; allele specific oligonucleotide; primer extension.
XX
OS Homo sapiens.
XX
PN WO200212562-A2.
XX
PD 14-FEB-2002.
XX
PF 06-AUG-2001; 2001WO-US24663.
XX
PR 04-AUG-2000; 2000US-223179P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Kliem SE, Koshy B;
XX
DR WPI; 2002-303982/34.
XX
PT Novel isolated human Phospholipase A2, Group IB pancreas
PT polynucleotide, for therapeutic purposes, for studying expression and
PT function of the polynucleotide and for expressing the phospholipase
PT protein -
XX
PS Claim 19; Page 13; 51pp; English.
XX
CC The invention relates to an isolated human Phospholipase A2, Group IB
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC polymorphic variant for a reference sequence for the PLA2G1B gene or
CC its fragment, or a polymorphic variant of a reference sequence for a
CC PLA2G1B cDNA or its fragment. Also included are haplotyping/genotyping
CC the PLA2G1B gene of an individual, predicting the haplotype pair for the
CC PLA2G1B gene of an individual, identifying an association between a trait
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC isolated genotyping oligonucleotide for detecting a polymorphism in the
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B
CC protein encoded by the first nucleotide sequence or by the polymorphic
CC variant sequence, an isolated polypeptide comprising a sequence which is
CC a polymorphic variant of a reference sequence for the PLA2G1B protein or
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC targeting PLA2G1B, a computer system for storing and analysing
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC gene. The PLA2G1B variant is useful in studying the expression and
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC screening for candidate drugs to treat diseases related to PLA2G1B
CC activity (e.g. pancreatitis and pancreatic cancer) and for
CC therapeutic purposes. The transgenic organism is useful for studying
CC expression of the PLA2G1B isogenes in vivo, for in vivo screening and
CC testing of drugs targeted against PLA2G1B protein, and for testing the
CC efficacy of therapeutic agents and compounds in a biological system.
CC The antibody is useful for studying the effect of the variation on the
CC biological activity of PLA2G1B as well as on the binding affinity of
CC candidate drugs targeting PLA2G1B. The PLA2G1B gene is located on
CC chromosome 12q23-q24.1. The present sequence is an allele specific
CC oligonucleotide (ASO) primer extension primer 3' end used to detect the
CC polymorphisms in PLA2G1B.
XX
SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 9 AGTATGA 3

RESULT 13
AAL41859
ID AAL41859 standard; DNA; 10 BP.
XX
AC AAL41859;

XX
DT 25-APR-2002 (first entry)
XX
DE Human GCNT1 allele specific primer extension oligo SEQ ID NO: 44.
XX
KW Human; glucosaminyl (N-acetyl) transferase 1, core 2; GCNT1; cancer;
KW gene therapy; haplotype; chromosome 9q13; SNP; primer; cytostatic;
KW single nucleotide polymorphism; ss.
XX
OS Homo sapiens.
XX
PN WO200204470-A2.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-US21451.
XX
PR 06-JUL-2000; 2000US-216281P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Finkel K, Koshy B;
XX
DR WPI; 2002-171696/22.
XX
PT Genetic variants of glucosaminyl (N-acetyl) transferase 1, core 2 gene
PT useful in studying expression and function of the protein, and for
PT screening drugs to treat diseases e.g. cancer -
XX
PS Claim 18; Page 14; 72pp; English.
XX
CC The present invention provides the gene, protein and cDNA sequences of
CC the human glucosaminyl (N-acetyl) transferase 1, core 1 (GCNT1). Also
CC identified are single nucleotide polymorphisms (SNPs) located within the
CC sequences. The sequences can be used in the treatment of GCNT1 related
CC diseases, including cancer. The present sequence is an allele specific
CC primer extension oligonucleotide for the GCNT1 gene, which is located on
CC chromosome 9q13.
XX
SQ Sequence 10 BP; 3 A; 1 C; 2 G; 4 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 1 AGTATGA 7

RESULT 14
AAI67680
ID AAI67680 standard; DNA; 10 BP.
XX
AC AAI67680;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human IL-8 gene polymorphism detecting primer.
XX
KW IL-8; interleukin; single nucleotide polymorphism; haplotyping; primer;
KW genotyping; cancer; chronic obstructive pulmonary disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO200183499-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US13957.
XX
PR 28-APR-2000; 2000US-200416P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2002-049333/06.
XX
PT Novel isolated human interleukin 8 polynucleotide, useful for
PT therapeutic purposes, comprises a sequence which is a polymorphic
PT variant of a reference sequence for interleukin 8 gene or its fragment
PT -
XX
PS Claim 18; Page 13; 52pp; English.
XX
CC The invention relates to novel single nucleotide polymorphisms in the
CC human interleukin 8 (IL-8) gene. Methods for haplotyping and genotyping
CC the IL-8 gene are also provided. The methods are useful for improving the
CC efficacy and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with IL-8 activity,
CC e.g., cancer and chronic obstructive pulmonary disease, to validate IL-8
CC as a candidate agent; in the design of clinical trials of candidate
CC drugs; to screen for compounds targeting IL-8 to treat a specific
CC conditions or disease associated with IL8 activity. The IL-8 gene is
CC useful in studying the expression and function of IL8, and in expressing
CC IL-8 protein for use in screening for candidate drugs to treat diseases
CC related to IL-8 activity. Sequences AAI67679-90 represent primers for
CC detecting IL-8 gene polymorphisms by primer extension.
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7
|||||||
Db 4 AGTATGA 10

RESULT 15
AAI67681/c
ID AAI67681 standard; DNA; 10 BP.
XX
AC AAI67681;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human IL-8 gene polymorphism detecting primer.
XX
KW IL-8; interleukin; single nucleotide polymorphism; haplotyping; primer;
KW genotyping; cancer; chronic obstructive pulmonary disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO200183499-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US13957.
XX
PR 28-APR-2000; 2000US-200416P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2002-049333/06.
XX
PT Novel isolated human interleukin 8 polynucleotide, useful for
PT therapeutic purposes, comprises a sequence which is a polymorphic
PT variant of a reference sequence for interleukin 8 gene or its fragment
PT -
XX
PS Claim 18; Page 13; 52pp; English.

XX
CC The invention relates to novel single nucleotide polymorphisms in the
CC human interleukin 8 (IL-8) gene. Methods for haplotyping and genotyping
CC the IL-8 gene are also provided. The methods are useful for improving the
CC efficacy and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with IL-8 activity,
CC e.g., cancer and chronic obstructive pulmonary disease, to validate IL-8
CC as a candidate agent; in the design of clinical trials of candidate
CC drugs; to screen for compounds targeting IL-8 to treat a specific
CC conditions or disease associated with IL8 activity. The IL-8 gene is
CC useful in studying the expression and function of IL8, and in expressing
CC IL-8 protein for use in screening for candidate drugs to treat diseases
CC related to IL-8 activity. Sequences AAI67679-90 represent primers for
CC detecting IL-8 gene polymorphisms by primer extension.
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGTATGA 7
              |||||||
Db         10 AGTATGA 4
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Job time : 118.151 secs